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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 165 Seconds
(without alignments)
309.408 Million cell updates/sec

Title: US-10-643-836-297

Perfect score: 703

Sequence: 1 MEGGAYAGKAGGAFDPYTL.....GEPHPAGTCTSTEGCPGP 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A_Geneseq_16Dec04:*

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	703	100.0	132	4	AAG89177 Human sec
2	582.5	82.9	191	8	ABM84393 Human dia
3	577	82.1	112	3	AG00298 Human sec
4	577	82.1	191	4	AAM39280 Human pol
5	577	82.1	211	8	ABM84391 Human dia
6	415.5	59.1	210	4	AAM41065 Human pol
7	415.5	59.1	210	4	AAM41066 Human pol
8	415.5	59.1	210	4	AAM41067 Human pol
9	413	58.7	182	4	AAM39281 Human pol
10	403.5	57.4	192	4	AAM39279 Human pol
11	403.5	57.4	234	8	ABM84392 Human dia
12	403	57.3	217	4	ABG26417 Novel hum
13	353	50.2	229	8	ADO19528 Human PRO
14	350.5	49.9	212	8	ABM84066 Human dia
15	305.5	43.5	225	8	ADP04527 Sea squir
16	296	42.1	204	8	ADM72128 Human NTR
17	296	42.1	224	2	AAM36516 Human syn
18	296	42.1	224	2	AAY41709 Human PRO
19	296	42.1	224	3	AAB44265 Human PRO
20	296	42.1	224	3	AAB24048 Human PRO
21	296	42.1	224	4	AAB64539 Gene 45 h
22	296	42.1	224	4	AAB64466 Human sec
23	296	42.1	224	4	AAB64540 Human sec
24	296	42.1	224	6	ABO25211 Novel hum
25	296	42.1	224	6	ABU72217 Novel hum

26	296	42.1	224	6	ABU84897 Human sec
27	296	42.1	224	6	ABU61095 Human PRO
28	296	42.1	224	6	ABU80364 Human sec
29	296	42.1	224	6	ADA24701 Novel hum
30	296	42.1	224	6	ABO19666 Novel hum
31	296	42.1	224	6	ADA12362 Human sec
32	296	42.1	224	6	ABO19557 Novel hum
33	296	42.1	224	6	ADB73668 Human PRO
34	296	42.1	224	7	ADB76384 Human PRO
35	296	42.1	224	7	ADC43810 Human sec
36	296	42.1	224	7	ADC61570 Human sec
37	296	42.1	224	7	ADC63534 Human sec
38	296	42.1	224	7	ADC66634 Human sec
39	296	42.1	224	7	ADC68758 Human sec
40	296	42.1	224	7	ADC62818 Human sec
41	296	42.1	224	7	ADC67883 Human sec
42	296	42.1	224	7	ADC41203 Human sec
43	296	42.1	224	7	ADC67258 Human sec
44	296	42.1	224	7	ADC62194 Human sec
45	296	42.1	224	7	ADC41827 Human sec
46	296	42.1	224	7	ADD45142 Human PRO
47	296	42.1	224	7	ADE54986 Human PRO
48	296	42.1	224	7	AD849196 Human sec
49	296	42.1	224	7	ADE35250 Human sec
50	296	42.1	224	7	ADE16364 Human sec

ALIGNMENTS

RESULT 1
AAG89177
ID AAG89177 standard; protein; 132 AA.

AC AAG89177;

DT 11-SEP-2001 (first entry)

DE Human secreted protein, SEQ ID NO: 297.

DE Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET.

OS Homo sapiens.

PN WO200142451-A2.

XX 14-JUN-2001.

XX 07-DEC-2000; 2000WO-IB001938.

XX 08-DEC-1999; 99US-0169629P.

XX 06-MAR-2000; 2000US-0187470P.

XX (GEST) GENSET.

PI Dumas Milne Edwards J, Bougueleret L, Jobert S;

DR WPI; 2001-367870/38.

DR N-PSDB; AAH64780.

XX Full length GENSET human nucleic acids encoding potentially secreted

PT proteins, useful in gene therapy and vaccination against a variety of

PT diseases, and for diagnosis of those diseases.

XX Claim 21; Page 828; 921pp; English.

CC The invention relates to full length GENSET human nucleic acids encoding

CC potentially secreted proteins. The nucleic acids and the polypeptides

CC they encode may be used in the prevention, treatment and diagnosis of

CC diseases associated with inappropriate GENSET gene expression. For

CC example, they be used to treat disorders associated with decreased

CC gene expression by rectifying mutations or deletions in a patient's

CC genome that affect the activity of GENSET or by supplementing the
 CC Patients own production of GENSET polypeptides. Conversely, antisense
 CC nucleic acid molecules may be administered to down regulate GENSET
 CC expression by binding with the cells' own genes and preventing their
 CC expression. The sense and antisense nucleic acids may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples, and hence to determine which
 CC patients may be in need of restorative therapy. The GENSET polypeptides
 CC may be used as antigens in the production of antibodies and in assays to
 CC identify modulators (agonists and antagonists) of GENSET polypeptide
 CC expression and activity. The present sequence is a GENSET polypeptide of
 CC the invention
 CC
 XX Sequence 132 AA;
 SQ
 Query Match 100.0%; Score 703; DB 4; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.3e-75;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
 DB 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
 QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 120
 DB 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 120
 QY 121 PCTESTEGCGPG 132
 DB 121 PCTESTEGCGPG 132
 RESULT 2
 ABM84393
 ID ABM84393 standard; protein; 191 AA.
 AC ABM84393;
 DT 18-NOV-2004 (first entry)
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:4642.
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 OS Homo sapiens.
 XX WO2004023973-A2.
 XX 25-MAR-2004.
 XX 12-SEP-2003; 2003WO-US028227.
 XX 12-SEP-2002; 2002US-0410259P.
 XX 12-SEP-2002; 2002US-0410260P.
 XX (INCY-) INCYTE CORP.
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthehorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
 PI Feralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX WPI: 2004-329368/30.
 DR N-PSDB; ACN43045.
 XX
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.

XX Claim 27; Page; 190pp; English.
 PS
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 CC
 XX Sequence 191 AA;
 SQ
 Query Match 82.9%; Score 582.5; DB 8; Length 191;
 Best Local Similarity 84.9%; Pred. No. 5.5e-61;
 Matches 118; Conservative 3; Mismatches 3; Indels 15; Gaps 3;
 QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
 DB 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
 QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 113
 DB 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSIDIGVSGEHPAGT 120
 QY 114 EHPAGTCTESTEG-CPG 131
 DB 121 QP-----TERRDGRSPG 132
 RESULT 3
 AAG00298
 ID AAG00298 standard; protein; 112 AA.
 AC AAG00298;
 XX 06-OCT-2000 (first entry)
 DT Human secreted protein, SEQ ID NO: 4379.
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 OS Homo sapiens.
 XX EP1033401-A2.
 XX 06-SEP-2000.
 XX 21-FEB-2000; 2000EP-00200610.
 XX 26-FEB-1999; 99US-0122487P.
 XX (GEST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI: 2000-500381/45.
 DR N-PSDB; AAC00304.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

Claim 13; SEQ ID NO 4379; 71pp + Sequence Listing; English.

PS The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors

XX Sequence 112 AA;

Query Match 82.1%; Score 577; DB 3; Length 112;
 Best Local Similarity 99.1%; Pred. No. 1.3e-60;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60
 DB 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60
 QY 61 YNRNPACSYGVAVGLAFITLCLLYLALDVYFPOISSVKDKKAVLSIDIGVS 112
 DB 61 YNRNPACSYGVAVGLAFITLCLLYLALDVYFPOISSVKDKKAVLSIDIGVS 112

RESULT 4
 AAM39280
 ID AAM39280 standard; protein; 191 AA.
 XX
 AC AAM39280;

22-OCT-2001 (first entry)
 Human polypeptide SEQ ID NO 2425.

Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 peripheral nervous system; neuropathy; central nervous system; CNS;
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia.

Homo sapiens.

WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US034263.

23-DEC-1999; 99US-00471275.

21-JAN-2000; 2000US-00488725.

25-APR-2000; 2000US-00552317.

20-JUN-2000; 2000US-00598042.

19-JUL-2000; 2000US-00620312.

03-AUG-2000; 2000US-00653450.

14-SEP-2000; 2000US-00662191.

19-OCT-2000; 2000US-00693036.

29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 Zhou F, Goodrich R, Drmanac RT;

DR N-PSDB; AAI58436.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

XX Example 4; SEQ ID NO 2425; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 191 AA;

Query Match 82.1%; Score 577; DB 4; Length 191;
 Best Local Similarity 99.1%; Pred. No. 2.5e-60;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60
 DB 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60
 QY 61 YNRNPACSYGVAVGLAFITLCLLYLALDVYFPOISSVKDKKAVLSIDIGVS 112
 DB 61 YNRNPACSYGVAVGLAFITLCLLYLALDVYFPOISSVKDKKAVLSIDIGVS 112

RESULT 5
 AAM84391
 ID AAM84391 standard; protein; 211 AA.

XX AAM84391;

18-NOV-2004 (first entry)

Human diagnostic and therapeutic pprotein SEQ ID NO:4640.

gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

Homo sapiens.

WO2004023973-A2.

25-MAR-2004.

12-SEP-2003; 2003WO-US028227.

12-SEP-2002; 2002US-0410259P.

12-SEP-2002; 2002US-0410260P.

(INCY-) INCYTE CORP.

Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kitron ES;
 Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JB, Gietzen D;
 Patury S, Shi X, Suarez CJ;
 WPI; 2004-329368/30.

DR N-PSDB; ACN43043.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 211 AA;
SQ
Query Match 82.1%; Score 577; DB 8; Length 211;
Best Local Similarity 99.1%; Pred. No. 2.8e-60;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLVRVSWLFSIVVFGSIVNNEGYNLSASEGEQFCI 60
DB 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLVRVSWLFSIVVFGSIVNNEGYNLSASEGEQFCI 60
QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDIGVS 112
DB 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDIGVS 112
RESULT 6
AAM41065
ID AAM41065 standard; protein; 210 AA.
XX
AC AAM41065;
XX
XX 22-OCT-2001 (first entry)
DT Human polypeptide SEQ ID NO 5996.
DE
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
PN
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000WO-US034263.
PF
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PSDB; AAI60221.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX Example 2; SEQ ID NO 5996; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
SQ Sequence 210 AA;
Query Match 59.1%; Score 415.5; DB 4; Length 210;
Best Local Similarity 66.4%; Pred. No. 5.9e-41;
Matches 89; Conservative 2; Mismatches 10; Indels 33; Gaps 3;
QY 31 VSW-----LFSIVVFGSIVNNEGYNLSASEGEQFCIYNRNPACSYGVAVGVLAFLTCL 83
DB 34 VSWRSRPGCELFSIVVFGSIVNNEGYNLSASEGEQFCIYNRNPACSYGVAVGVLAFLTCL 93
QY 84 LYLALDVYFPQISSVKDRKAVLSDIG-VSGPFPAG----- 119
DB 94 LYLALDVYFPQISSVKDRKAVLSGHPVVSSEGEHPAPFAWFLWFTGDCSYLANQWQVSKP 153
QY 120 --TPCTESTGCPG 131
DB 154 KDNPLNEGTDASPG 167
RESULT 7
AAM41066
ID AAM41066 standard; protein; 210 AA.
XX
AC AAM41066;
XX
XX 22-OCT-2001 (first entry)
DT Human polypeptide SEQ ID NO 5997.
DE
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
PN
XX

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

XX Homo sapiens.
OS WO200153312-A1.
PN 26-JUL-2001.
PD
PX 26-DEC-2000; 2000WO-US034263.
PY 23-DEC-1999; 99US-00471275.
PZ 21-JAN-2000; 2000US-00488725.
QA 25-APR-2000; 2000US-00552317.
QB 20-JUN-2000; 2000US-00598042.
QC 19-JUL-2000; 2000US-00620312.
QD 03-AUG-2000; 2000US-00653450.
QE 14-SEP-2000; 2000US-00662191.
QF 19-OCT-2000; 2000US-00693036.
QG 29-NOV-2000; 2000US-00727344.
QH (HYSE-) HYSEQ INC.
QI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
QJ Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
QK Zhou P, Goodrich R, Drmanac RT;
QL WPI; 2001-442253/47.
QM N-PSDB; AA160223.
QN Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
QO Example 2; SEQ ID NO 5997; 10078pp; English.
QP The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Actin/inhibit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Sequence 210 AA;
Query Match 59.1%; Score 415.5; DB 4; Length 210;
Best Local Similarity 66.4%; Pred. No. 5.9e-41;
Matches 89; Conservative 2; Mismatches 10; Indels 33; Gaps 3;

QY 31 VSW-----LFSIVVFGSIVNEGYLNASGEQFCIYNRNPNACSYGVAVGLAFTCL 83
DB 34 VSWRSRPGCELFSIVVFGSIVNEGYLNASGEQFCIYNRNPNACSYGVAVGLAFTCL 93
QY 84 LYLALDVYPFOISSVKDRKKAVLSDTIG-VSGEPHPAG----- 119
DB 94 LYLALDVYPFOISSVKDRKKAVLSGHPVVSGBPHPAAFWFLWFTGDSCYLANQOVSKP 153
QY 120 --TPCTESTEGCGP 131
DB 154 KDNPLNEGTDASP 167

RESULT 8
AAM41067 standard; protein; 210 AA.
AC AAM41067;
XX 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 5998.
XX

26-JUL-2001.
26-DEC-2000; 2000WO-US034263.
23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00662191.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
Zhou P, Goodrich R, Drmanac RT;
WPI; 2001-442253/47.
N-PSDB; AA160222.
Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
Example 2; SEQ ID NO 5997; 10078pp; English.
The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Actin/inhibit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Sequence 210 AA;
Query Match 59.1%; Score 415.5; DB 4; Length 210;
Best Local Similarity 66.4%; Pred. No. 5.9e-41;
Matches 89; Conservative 2; Mismatches 10; Indels 33; Gaps 3;

QY 31 VSW-----LFSIVVFGSIVNEGYLNASGEQFCIYNRNPNACSYGVAVGLAFTCL 83
DB 34 VSWRSRPGCELFSIVVFGSIVNEGYLNASGEQFCIYNRNPNACSYGVAVGLAFTCL 93
QY 84 LYLALDVYPFOISSVKDRKKAVLSDTIG-VSGEPHPAG----- 119
DB 94 LYLALDVYPFOISSVKDRKKAVLSGHPVVSGBPHPAAFWFLWFTGDSCYLANQOVSKP 153
QY 120 --TPCTESTEGCGP 131
DB 154 KDNPLNEGTDASP 167

RESULT 8
AAM41067 standard; protein; 210 AA.
AC AAM41067;
XX 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 5998.
XX

RESULT 9
AAM39281
ID AAM39281 standard; protein; 182 AA.
XX
AC AAM39281;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2426.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
(HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB; AAI58437.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2426; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 182 AA;
Query Match 58.7%; Score 413; DB 4; Length 182;
Best Local Similarity 98.8%; Pred. No. 9.7e-41;
Matches 80; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

32 SWLSFIVVFGSIVNEGYNLSAGEGFCIYNRPNACS YGVAVGVLAFITCLLYALDYY 91

Db 23 SWLSFIVVFGSIVNEGYNLSAGEGFCIYNRPNACS YGVAVGVLAFITCLLYALDYY 82
QY 92 FPOISSVKDRKKAVLSDIGVS 112
Db 83 FPOISSVKDRKKAVLSDIGVS 103
RESULT 10
AAM39279
ID AAM39279 standard; protein; 192 AA.
XX
AC AAM39279;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2424.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
(HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB; AAI58435.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2424; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX

```

CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 234 AA;
Query Match 57.4%; Score 403.5; DB 8; Length 234;
Best Local Similarity 91.0%; Pred. No. 1.8e-39;
Matches 81; Conservative 1; Mismatches 0; Indels 7; Gaps 1;
QY 31 VSW-----LFSIVFGSIVNEGYLNSASEGQFCIYNNPNACSYGVAVGLAFLTCL 83
Db 25 VWSRSPGCGELFSIVVFGSIVNEGYLNSASEGEEFCIYNNPNACSYGVAVGLAFLTCL 84
QY 84 LYIALDVYFPQISSVKDRKKAVLSDIGVS 112
Db 85 LYIALDVYFPQISSVKDRKKAVLSDIGVS 113
RESULT 12
ABG26417
ID ABG26417 standard; protein; 217 AA.
XX
XX ABG26417;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #26408.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US0008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS90604.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX
XX Claim 20; SEQ ID NO 56776; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridization probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

```

CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 217 AA;

Query Match 57.3%; Score 403; DB 4; Length 217;
 Best Local Similarity 97.4%; Pred. No. 1.9e-39;
 Matches 74; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 56 EQFCINRNPNACSYGVAVGVLAFLTCLLYLALDVYFPOISSVKDRKKAVLSDIGVSGEP 115
 :|||||
 DB 1 KSFICINRNPNACSYGVAVGVLAFLTCLLYLALDVYFPOISSVKDRKKAVLSDIGVSGEP 60
 :|||||

QY 116 HPAGTCTESTGCPG 131
 |||||
 DB 61 HPAGTCTESTGCPG 76

RESULT 13
 ADO19528
 ID ADO19528 standard; protein; 229 AA.
 XX
 AC ADO19528;
 XX
 DT 12-AUG-2004 (first entry)
 DE
 DE Human PRO polypeptide #229.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PR (GETH) GENENTECH INC.
 PA
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 XX
 WPI: 2004-420067/39.
 DR N-PSDB; ADO19527.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7; SEQ ID NO 458; 1731pp; English.

CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,

CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX
 SQ Sequence 229 AA;

Query Match 50.2%; Score 353; DB 8; Length 229;
 Best Local Similarity 58.4%; Pred. No. 2e-33;
 Matches 66; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAPDPYTLVRQPHILRVSWLFSIVVFGSIVNNGYNSASEGEQFCI 60
 :|||||
 DB 1 MEGASFGAGAGALDPVSFARPTLLRVSASWFSIAVFGPIVNEGIVNTDSGPRLRCV 60
 :|||||

QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPOISSVKDRKKAVLSDIGVSG 113
 :|||||
 DB 61 FNGNAGACRFGVGLGFLACAAFLLDVRFQISSVRRRRRLLDLGFSG 113

RESULT 14
 ABM84066
 ID ABM84066 standard; protein; 212 AA.
 XX
 AC ABM84066;
 XX
 DT 18-NOV-2004 (first entry)
 DE
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:4315.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marianovic MM, Shen F;
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CU;
 XX
 WPI: 2004-329368/30.
 DR N-PSDB; ACN42718.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 212 AA;

Query Match 49.9%; Score 350.5; DB 8; Length 212;
Best Local Similarity 55.3%; Pred. NO. 3.5e-33;
Matches 68; Conservative 20; Mismatches 32; Indels 3; Gaps 1;

QY 1 MEGAGYAGKAGGAGFDPYTLVROPHITLRVSVLFSIVVFGSIVNEGYNLSASEGQFCI 60

Db 1 MEGAGYAGKAGGAGALDPVSFARRPQTLIRVASVWFSIAVFGPIVNGYVNTDGPRLRCV 60

QY 61 YNRNPNACSYGVAVGLAFUTCLLYLALDVFQISSVKDRKAVLSDIGVSGE---PHP 117

Db 61 FNGNAGCRFGVALGLGAFACAFLLDVRFOQISSVRRDRRAVLLDLGFQWQRTAPGP 120

QY 118 AGT 120

Db 121 ATT 123

RESULT 15

ADP04527
ID ADP04527 standard; protein; 225 AA.

XX
AC ADP04527;

DT 29-JUL-2004 (first entry)

XX Sea squirt protein with tissue specific expression in development Seq122.

XX sea squirt; regeneration medicine; gene therapy; cell proliferation;
XX differentiation; reproduction; environmental measurement; water survey.

XX Ciona intestinalis.

XX JP2004057129-A.

XX 26-FEB-2004.

XX 31-JUL-2002; 2002JP-00222593.

XX 31-JUL-2002; 2002JP-00222593.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2004-287079/27.

XX N-PSDB; ADP04526.

XX Novel gene cluster which is specifically expressed in tissue or organ
XX during developmental phase of sea squirt, useful for elucidation of
XX mechanism of development of tissue or organ of sea squirt.

XX Claim 1; SEQ ID NO 122; 1846pp; Japanese.

XX This invention relates to novel genes and the encoded proteins thereof
XX that are derived from the sea squirt Ciona intestinalis. Specifically, it
XX refers to those genes that are expressed in the tissues or organs of the
XX sea squirt during its developmental phase. The present invention
XX describes the identification of these genes as useful for elucidation of
XX the mechanism of development and hence for developing regeneration
XX medicines and gene therapy techniques. Accordingly, they can be used in
XX the research of various genetic diseases, as well as the analysis of cell
XX proliferation, differentiation and reproduction. Furthermore, such
XX compositions can be useful for environmental measurements and water
XX surveys, particularly for sea water surveys, and also for the preparation
XX of transformed sea squirt for improving edibility of sea squirt such as
XX Halocynthia roretzi. This polypeptide sequence is a sea squirt protein

CC sequence that has tissue specific expression during development, given in
CC an exemplification of the invention.

XX Sequence 225 AA;

Query Match 43.5%; Score 305.5; DB 8; Length 225;
Best Local Similarity 51.8%; Pred. NO. 9.2e-28;
Matches 58; Conservative 22; Mismatches 27; Indels 5; Gaps 1;

QY 2 EGGAYGAGKAGGAGFDPYTLVROPHITLRVSVLFSIVVFGSIVNEGYNLSASEGQFCIY 61

Db 3 QGGAYGAGKAGGAGFDPYTLVROPHITLRVSVLFSIVVFGSIVVFGSIVVFGSIVVFGSIV 57

QY 62 NRPNACSYGVAVGLAFUTCLLYLALDVFQISSVKDRKAVLSDIGVSG 113

Db 58 GDDPNACHYGAIVGLAFITISTVFFAALDVFPSISSAERKKVVMADVFFSG 109

RESULT 16

ADM72128
ID ADM72128 standard; protein; 204 AA.

XX ADM72128;

DT 03-JUN-2004 (first entry)

XX Human NTRAN polypeptide (clone ID 7520846CD1).

XX NTRAN; neurotransmission-associated protein; cytostatic;
XX antiarteriosclerotic; anti-HIV; antiallergic; cerebroprotective;
XX antiparkinsonian; anticonvulsant; dermatological; nootropic;
XX neuroprotective; antiinflammatory; antithyroid; antiarthritic; anorectic;
XX cardiant; hypotensive; hepatotropic; gene therapy; human.

XX Homo sapiens.

XX WO2004022705-A2.

XX 18-MAR-2004.

XX 02-SEP-2003; 2003WO-US027411.

XX 04-SEP-2002; 2002US-0408383P.

XX 05-SEP-2002; 2002US-0408781P.

XX 26-SEP-2002; 2002US-0414221P.

XX 13-NOV-2002; 2002US-0426483P.

XX 06-DEC-2002; 2002US-0431566P.

XX 17-DEC-2002; 2002US-0434317P.

XX 03-JAN-2003; 2003US-0437763P.

XX (INCY-) INCYTE CORP.

XX Lee SY, Elliott VS, Hafalia AJA, Burford N, Sprague WW;

XX Griffin JA, Yang YG, Chawla NK, Baughn MR, Becha SD, Khare R;

XX Thornton MB, Mason PM, Gietzen KJ, Ison CH, Marquis JP, Swarnakar A;

XX Ramkumar J, Jin P, Richardson TW, Tran UK;

XX WPI; 2004-269571/25.

XX N-PSDB; ADM72159.

XX New human neurotransmission-associated proteins and polynucleotides for
XX diagnosing, preventing or treating diseases or conditions associated with
XX aberrant protein expression, e.g. cancer, hepatitis, AIDS, obesity or
XX stroke.

XX Claim 1; SEQ ID NO 9; 216pp; English.

XX The invention relates to human neurotransmission-associated proteins
XX (NTRAN) and encoding polynucleotides. The NTRAN polypeptides can be
XX expressed by standard recombinant methodology. The polypeptides and
XX polynucleotides are useful in diagnosing, preventing or treating diseases
XX or conditions associated with the decreased expression or overexpression
XX of NTRAN, such as autoimmune/inflammatory, cardiovascular, neurological,


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PD 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US014926.
XX
XX 11-JUN-1999; 99US-0138628P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
XX
XX WPI; 2001-025337/03.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
XX Disclosure; Page 582-583; 593pp; English.
XX
XX The polynucleotide sequences given in AAF32699 to AAF32747 encode the
XX human secreted proteins given in AAB64422 to AAB64470. AAB64471 to
XX AAB64548 represent human secreted polypeptide sequences and proteins
XX homologous to them, which are given in the exemplification of the present
XX invention. Human secreted proteins have activities based on the tissues
XX and cells the genes are expressed in. Examples of activities include:
XX antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
XX cytotatic; cardiant; vasotropic; cerebroprotective; neurotropic;
XX neuroprotective; antibacterial; virucide; fungicide; and
XX ophthalmological. The polynucleotides and polypeptides can be used to
XX prevent, treat or ameliorate a medical condition in e.g. humans, mice,
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
XX in diagnosing a pathological condition or susceptibility to a
XX pathological condition. Disorders which are diagnosed or treated include
XX autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
XX disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
XX e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
XX angiogenesis, nervous system disorders e.g. Alzheimer's disease,
XX infections caused by bacteria, viruses and fungi and ocular disorders
XX e.g. corneal infection. The polypeptides can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin aging due to
XX sunburn, to maintain organs before transplantation, for supporting cell
XX culture of primary tissues, to regenerate tissues and in chemotaxis. The
XX polypeptides can also be used as a food additive or preservative to
XX increase or decrease storage capabilities. AAF32699 to AAF32698 and
XX AAB64421 represent sequences used in the exemplification of the present
XX invention
XX
XX Sequence 224 AA;
XX
XX Query Match 42.1%; Score 296; DB 4; Length 224;
XX Best Local Similarity 48.6%; Pred. No. 1.3e-26;
XX Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
XX
XX 1 MEGAYGAGKAGGAFDPYTLVRQHTILRVWSLFSIVVFGSVINSGYLSASGEQFCI 60
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 1 MESGAYGAAGKAGGSFDRRLFTQPVVARAVCLVFLVFSICLYGEGYSNAHESKQMYCV 60
XX
XX 61 YNRPNACSYGVAVGLAFLTCLLYLALDVFPQISSVKDRKXVLSDI 109
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKVLVIGDL 109
XX
XX RESULT 22
XX AAB64466
XX ID AAB64466 standard; protein; 224 AA.
XX
XX XX AAB64466;
XX
XX 23-MAR-2001 (first entry)
XX
XX Human secreted protein sequence encoded by gene 45 SEQ ID NO:104.
XX
XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
```


(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DA,
 PI Ferrarà N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen
 PI Goddard A, Godowski PU, Grimaldi JC, Gurney AL, Hullan KJ,
 PI Kljavin Iu, Kuo SS, Napier NA, Pan J, Paoni NF, Roy MA,
 PI

PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-328499/31.
DR N-PSDB; ACA71759.
XX
PT New isolated PRO polypeptides e.g. PRO213, PRO274 and PRO300, for use as
PT pharmaceuticals, diagnostics, biosensors and bioreactors, for identifying
PT modulators of receptor-ligand interactions.
XX
XX Claim 12; SEQ ID NO 162; 55pp; English.
PS
XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide. The PRO polypeptide is useful
CC in PRO polypeptide detection methods. The PRO polypeptide is useful for
CC linking a bioactive molecule to a cell. The PRO polypeptide or an
CC antibody against it is useful for modulating a biological activity of a
CC cell. The PRO polypeptide is useful in industrial applications including
CC pharmaceuticals, diagnostics, biosensors and bioreactors. The PRO
CC polypeptide is also useful as a thrombolytic agent, interferon,
CC interleukin, erythropoietin, colony stimulating factor and other
CC cytokines. The PRO polypeptide is useful for treating disease such as
CC cancer e.g. colorectal carcinoma; apoptosis related conditions e.g. AIDS,
CC amyotrophic lateral sclerosis; inflammatory disease e.g. asthma,
CC atherosclerosis; neurodegenerative disease e.g. Alzheimer's disease,
CC Parkinson's disease; cardiovascular disease e.g. hypertension and
CC myocardial ischaemia; kidney disease e.g. renal failure and
CC glomerulonephritis; lung disease e.g. pulmonary hypertension, bronchial
CC asthma; gastrointestinal disorders e.g. gastric ulcer and inflammatory
CC bowel disease; reproductive disorders e.g. premature labour and
CC pre-eclampsia; carcinogenesis. The present sequence represents the amino
CC acid sequence of a PRO polypeptide of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification but
CC was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20020177553
XX
SQ Sequence 224 AA;

Query Match 42.1%; Score 296; DB 6; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.3e-26;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MEGAYGAGKAGAFDPTLVROPHTTLRVVSLFSLVFGSVNKGYNLSASEGQFCI 60
Db 1 MEGAYGAGKAGSFDLRRLFTQPVVARVCLVFLVFPSCIYGGYNAHESKQMYCV 60

Qy 61 YNRNPACSYGAVGVLAFLTCLLYLALDLYFPQISSVKDRKXVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFSLASAFFLVVDAYFPQISNATDKYLVIGDL 109

RESULT 27
ABU61095
ID ABU61095 standard; protein; 224 AA.
XX
AC ABU61095;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human PRO615 polypeptide.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
KW cardiac insufficiency; nervous system disorder; kidney disorder;
KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
KW genetic disorder; cytostatic; antidiabetic; antiinflammatory;
KW antiarthritic; anti-tumour; vulnery; antianaemic; dermatological;
KW cardiant.
XX
OS Homo sapiens.
XX
XX US2002169284-A1.
XX
XX 14-NOV-2002.
PD

XX
PF 16-OCT-2001; 2001US-00978697.
XX
XX 26-MAY-1981; 81US-00267213.
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 26-JUN-1998; 98US-00105413.
PR 07-OCT-1998; 98US-00168978.
PR 02-NOV-1998; 98WO-US021141.
PR 07-OCT-1998; 98WO-US0184216.
PR 06-NOV-1998; 98US-00187368.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-00218517.
PR 05-JAN-1999; 99WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00285686.
PR 12-MAR-1999; 99WO-US005190.
PR 12-APR-1999; 99US-00284291.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380142.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.
 20-DEC-2000; 2000WO-US034956.
 28-FEB-2001; 2001WO-US006520.
 22-MAR-2001; 2001US-00816744.
 22-MAR-2001; 2001US-00816920.
 22-MAR-2001; 2001WO-US009552.
 10-MAY-2001; 2001US-00854208.
 10-MAY-2001; 2001US-00854280.
 25-MAY-2001; 2001WO-US017092.
 01-JUN-2001; 2001US-00872035.
 01-JUN-2001; 2001WO-US017800.
 05-JUN-2001; 2001US-00874503.
 14-JUN-2001; 2001US-00882636.
 19-JUN-2001; 2001US-00886342.
 20-JUN-2001; 2001WO-US015692.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 30-JUL-2001; 2001US-00918585.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI; 2003-288163/28.
 DR N-PSDB; ABX92399.
 XX
 XX
 XX Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies.
 XX
 PS Claim 12; Fig 61; 459pp; English.
 PS
 XX
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The bioactive molecule maybe a
 CC toxin, radiolabel or antibody, and causes apoptosis or death of the cell.
 CC The PRO polypeptides are useful for treating immune disorders, diabetes
 CC or hyper- or hypo-insulinaemia, cardiac insufficiency, nervous system
 CC disorders, kidney disorders, bone and cartilage disorders or arthritis,
 CC tumours, and wound healing. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and gene
 CC mapping, in the generation of antisense RNA and DNA, in the preparation
 CC of PRO polypeptides, for generating transgenic animals or knockout
 CC animals, for the genetic analysis of individuals with genetic disorders,
 CC and in gene therapy. ABU61071-ABU61164 represent the human PRO
 CC polypeptides of the invention. Note: The sequence data for this patent
 CC was obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/peipsDIDEntry.html
 XX
 SQ Sequence 224 AA;
 Query Match 42.1%; Score 296; DB 6; Length 224;
 Best Local Similarity 48.6%; Pred. No. 1.3e-26;
 Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
 Oy 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSVWLSFISIVFGSIVNEGILNASGEQFCI 60
 Db 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSVWLSFISIVFGSIVNEGILNASGEQFCI 60
 Oy 61 YNRPNACSYGVGVGLAFLTCLLYLALDVFFPOISSVKDKKAVLSDI 109
 Db 61 FNRNEDACRYGSAIGVGLAFLAFLVVDVDFPOISSATDKRKLVLIGDL 109
 ABUS0364
 ID ABUS0364 standard; protein; 224 AA.
 XX
 AC ABUS0364;
 XX
 DT 24-JUN-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO615.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; malignancy; cancer;
 KW ovarian cancer; colorectal cancer; sarcoma; leukaemia; lymphoma;
 KW inflammatory disease; necrosis; atherosclerosis; infertility;
 KW premature aging; psoriasis; inflammation; inflammatory disease; renal disease;
 KW arthritis; immune-mediated alopecia; stroke; encephalitis; hepatitis;
 KW multiple sclerosis; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US2003004102-A1.
 PN
 XX
 PD 02-JAN-2003.
 XX
 XX 15-OCT-2001; 2001US-00978189.
 PF
 XX 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 17-MAR-1998; 98US-00040220.
 PR 20-MAR-1998; 98US-007886P.
 PR 20-MAR-1998; 98US-0078910P.
 PR 20-MAR-1998; 98US-0078936P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 26-MAR-1998; 98US-0079656P.
 PR 27-MAR-1998; 98US-0079663P.
 PR 27-MAR-1998; 98US-0079664P.
 PR 27-MAR-1998; 98US-0079689P.
 PR 27-MAR-1998; 98US-0079728P.
 PR 27-MAR-1998; 98US-0079786P.
 PR 30-MAR-1998; 98US-0079920P.
 PR 30-MAR-1998; 98US-0079923P.
 PR 26-JUN-1998; 98US-00105413.
 PR 07-OCT-1998; 98US-00168978.
 PR 07-OCT-1998; 98WO-US021141.
 PR 02-NOV-1998; 98US-00184216.
 PR 08-NOV-1998; 98US-00187368.
 PR 20-NOV-1998; 98WO-US024855.
 PR 07-DEC-1998; 98US-00202054.
 PR 22-DEC-1998; 98US-00218517.
 PR 05-JAN-1999; 99WO-US000106.
 PR 05-MAR-1999; 99US-00254465.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-00265686.
 PR 10-MAR-1999; 99WO-US005190.
 PR 12-MAR-1999; 99US-00267213.
 PR 12-APR-1999; 99US-00284291.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380142.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.

PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US0113705.
PR 22-MAY-2000; 2000WO-US0114042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00818744.
PR 22-MAR-2001; 2001US-00818920.
PR 10-MAY-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
PI Ferrera N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI: 2003-341189/32.
DR N-PSDB; ACA6140.
XX
XX
XX New genes and secreted and transmembrane polypeptides (e.g. PRO337 or
PT PRO1559), useful for treating or diagnosing e.g. cancers,
PT atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple
PT sclerosis in mammals.
XX
XX
XX Claim 12; Fig 61; 460pp; English.
XX
XX The invention relates to a new isolated nucleic acid molecule comprises a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic

CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioeffectors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukaemia or lymphoma), inflammatory disease,
CC necrosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory disease, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence represents a PRO polypeptide
XX
XX
XX Sequence 224 AA;
Query Match 42.1%; Score 296; DB 6; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.3e-26;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPYTLVPOPHHTILRVVSWLPSIVVFGSIVNEGYNLSASEGEQFCI 60
Db 1 MESSGAYGAAGAGGSDLRFRFTQPVVAKAVCLVFLVFCIYGEYSNAHESQMYCV 60
QY 61 YNRNPACSYGAVGVLAFLTCLLYLALDVVFPFQISSVKDKKAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLIGDL 109
RESULT 29
ADA24701
ID ADA24701 standard; protein; 224 AA.
XX
XX AC ADA24701;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO615.
XX
XX KW Human; secreted and transmembrane protein; PRO; tissue typing;
KW chromosome identification; vaccine; cancer; retinal disorder;
KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
KW wound healing; obesity; diabetes; hearing loss;
KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
KW haemoglobin associated disorder.
XX
XX OS Homo sapiens.
XX
XX PN US2003050241-A1.
XX
XX PD 13-MAR-2003.
XX
XX PF 16-OCT-2001; 2001US-00978564.
XX
XX PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0065364P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
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PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
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PR 31-MAR-1998; 98US-0080107P.
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PR 01-APR-1998; 98US-0080327P.
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PR 01-APR-1998; 98US-0080333P.
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PR 08-APR-1998; 98US-0081049P.
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PR 08-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
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PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083366P.
PR 28-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
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PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083554P.
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PR 29-APR-1998; 98US-0083559P.
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PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084415P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
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PR 07-MAY-1998; 98US-0084639P.
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PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.

PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 01-JUL-1998; 98US-0094651P.
PR 30-JUL-1998; 98US-0100038P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98US-0109304P.
PR 20-NOV-1998; 98US-0109304P.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-0113621P.
PR 08-MAR-1999; 99WO-US000106.
PR 10-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99WO-US005190.
PR 29-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US011705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI KJjavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-521814/49.
DR N-PSDB; ADA24700.


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PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094851P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 23-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 03-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 27-JUL-1999; 99US-0142680P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
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PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WL;
XX
XX WPI; 2003-503575/47.
XX N-PSDB; ACD29741.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
XX activity of cell expressing the polypeptide, identifying agonists or
PT

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PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 12; Fig 61; 459pp; English.

XX The invention describes an isolated, secreted and transmembrane
 CC polypeptide, termed PRO polypeptide (I). (I) is useful for detecting
 CC PRO4993, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
 CC linking a bioactive molecule to a cell expressing the above polypeptides.
 CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
 CC cell death. (I) is useful as therapeutic agent, in medical and industrial
 CC applications e.g. for treating neuropathy, especially peripheral
 CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
 CC Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinemia,
 CC Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's

Query Match 42.1%; Score 296; DB 6; Length 224;

Best Local Similarity 48.6%; Pred. No. 1.3e-26;

Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

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Db 1 MESGAYGAAGAGGFDLRRFLTPQVVARAVCLVAFALIVFSCIYGEYSNAHESKQMYCV 60

QY 61 YNRPNACSYGVAVGVLAELTCLLYLALDVYFPOISSVKDRKKAFLSDI 109

Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVDVAYFPQISNATDRKYLVIIGDL 109

RESULT 31

ADAL2362

ID ADAL2362 standard; protein; 224 AA.

XX ADAL2362;

XX 06-NOV-2003 (first entry)

DT Human secreted/transmembrane polypeptide PRO615.

DE inflammatory disease; organ failure; atherosclerosis; cardiac injury;

XX infertility; birth defect; premature aging; AIDS; cancer;

KW diabetic complication; tissue typing; human.

XX Homo sapiens.

OS US2003055216-A1.

PN 20-MAR-2003.

XX 17-OCT-2001; 2001US-00978824.

XX 21-MAY-1996; 96US-0018049P.

PR 17-OCT-1997; 97US-0062250P.

PR 03-NOV-1997; 97US-0064249P.

PR 13-NOV-1997; 97US-0065311P.

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PR	01-JUL-1998;	98US-0091359P.	PR	01-JUN-2001;	2001WO-US017800.
PR	30-JUL-1998;	98US-0094651P.	PR	05-JUN-2001;	2001US-00874503.

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PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US015692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

Query Match 42.1%; Score 296; DB 6; Length 224;
Best Local Similarity 48.6%; Pred. NO. 1.3e-26;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

OY 1 MEGGAYGAGKAGGAFDYLVRPHITLIRVSVLFSIVVFGSIVNRCYLNSASEGEQFCI 60
DB 1 MESSGAYGAAGKAGGFDLRRFLTPQVVARAVCLVFLVIFSCYIGEGYNASHESKOMYCV 60

OY 61 YNENPNACSGVAGVGLAFITCLLLXALDVRPQISSVKDRKKAIVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLLVDVAYFPQISNATDRKYLVIQDL 109

RESULT 32
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ID ABO19557 standard; protein; 224 AA.
XX
AC ABO19557;
XX
DT 27-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane polypeptide #25.
XX
KW Human; secreted and transmembrane protein; PRO; viral infection;
KW tumour growth; retinal disorder; injury; sight loss;
KW retinitis pigmentosa; age-related macular degeneration;
KW sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangier disease;
KW Refsum's disease.
XX
OS Homo sapiens.
XX
PN US2003049633-A1.
XX
PD 13-MAR-2003.
XX
PP 16-OCT-2001; 2001US-00978585.
XX
PR 17-OCT-1997; 97US-0062250P.
PR 03-NOV-1997; 97US-0064249P.
PR 13-NOV-1997; 97US-0065311P.
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PR 11-MAR-1998; 98US-0077632P.
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 PR 29-MAR-1999; 99US-0126773P.
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 PR 26-APR-1999; 99US-0131022P.
 PR 28-APR-1999; 99US-0131445P.
 PR 14-MAY-1999; 99US-00311832.
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 PR 16-JUN-1999; 99US-0139557P.
 PR 23-JUN-1999; 99US-0141037P.
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 PR 27-NOV-2000; 2000US-00723749.
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 KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
 KW chromosome mapping; gene mapping; genetic disorder; septic shock;
 KW antibacterial; immunosuppressive; neuroprotective.
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(GETH) GENENTECH INC.

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PR			PR	08-APR-1998;	98US-0081071P.	
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PA	(GETH) GENENTECH INC.					
XX	Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;					
PI						

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Best Local Similarity 48.6%; Pred. No. 1.3e-26;
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 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
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 PR 30-JUL-2001; 2001US-00918585.
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 PA (GETH) GENENTECH INC.
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 PI Ashtenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DJ;
 Query Match 42.1%; Score 296; DB 7; Length 224;
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 Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
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 DB 1 MESGAYGAAGAGGSGFLRRFLTQPQVARAVCLVFALIVFCIYGEVSNHESKQMYCV 60
 QY 61 YNRNPNACSYGAVGVGLAFLTCLLLALDVPVFPQISSVKDKKAVLSDI 109
 DB 61 FNRNEDACRYGSAIGVLAFLASAPFLVVDAYFPQISNATDRKYLVIIGDL 109
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 AC ADC62818;
 XX
 DT 18-DEC-2003 (first entry)
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 XX
 KW Human; secreted protein; transmembrane protein; PRO; cytostatic;
 KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
 KW auditory; tumour growth; retinal disorder; sports-related joint problem;
 KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 KW wound healing; hearing loss.
 XX
 OS Homo sapiens.
 XX
 PN US2003068648-A1.
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 PD 10-APR-2003.
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 PF 25-OCT-2001; 2001US-00013921.
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 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 20-MAR-1998; 98US-0078886P.
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 PR 20-MAR-1998; 98US-0078939P.

Claim 12: SEO ID NO 162: 467pp; English.

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PR 07-OCT-1998; 98WO-US021141.
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PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
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PR 14-MAY-1999; 99WO-US010733.
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PR 30-DEC-1999; 99WO-US031243.
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PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 21-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
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PR 20-DEC-2000; 2000WO-US034956.
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PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PA (GETH) GENENTECH INC.
XX Ashkenazi A, Baker KP, Botstein D, Desnovers L, Eaton DL;
XX Ferrera N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Raoni NF, Roy MA, Shelton DL;
PI Stewart TA, Thomas D, Williams PW, Wood WI;
XX WPI; 2003-743806/70.
DR N-PSDB; ADC41202.
XX Novel isolated secreted and transmembrane PRO polypeptides, useful in the
PT preparation of a medicament for treating a condition responsive to the
PT polypeptide, and as therapeutic agents e.g. vaccines.
XX Claim 12; SEQ ID NO 162; 466pp; English.
PS

XX	CC	The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80% amino acid sequence identity to an amino acid sequence chosen from 94 fully defined sequences as given in the specification (including PRO lacking its associated signal peptide), a PRO extracellular domain with or without its associated signal peptide). Also included are nucleic acids encoding the PRO proteins mentioned above, a vector comprising a PRO nucleic acid, a host cell comprising the vector and producing PRO, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. PRO337 polypeptide is useful for detecting a PRO4993 polypeptide in a sample suspected of containing PRO4993 polypeptide.
Query Match	42.1%; Score 296; DB 7; Length 224;	
Best Local Similarity	48.6%; Pred. No. 1.3e-26;	
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;		
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AC		
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DT	18-DEC-2003 (first entry)	
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KW	vulnery; virucide; neuroprotective; cytostatic; gene therapy;	
KW	tumour cell proliferation inhibitor;	
KW	secreted and transmembrane protein; PRO; viral infection; wound healing;	
KW	tissue growth; muscle generation; muscle regeneration;	
KW	amyotrophic lateral sclerosis; neuropathy; AIDS-associated neuropathy;	
KW	diabetic peripheral neuropathy; chromosome identification; antagonist;	
KW	tissue typing; immunohistochemical staining.	
OS	Homo sapiens.	
XX		
PN	US2003073131-A1.	
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PD	17-APR-2003.	
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PF	25-OCT-2001; 2001US-00016177.	
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PR	17-OCT-1997; 97US-0062250P.	
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PR	21-NOV-1997; 97US-0066364P.	
PR	10-MAR-1998; 98US-0077450P.	
PR	11-MAR-1998; 98US-0077632P.	
PR	11-MAR-1998; 98US-0077641P.	
PR	11-MAR-1998; 98US-0077649P.	
PR	12-MAR-1998; 98US-0077791P.	
PR	13-MAR-1998; 98US-0078004P.	
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PR	20-MAR-1998; 98US-0078910P.	
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PR	20-MAR-1998; 98US-0078939P.	
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PR	26-MAR-1998; 98US-0079656P.	
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 PR 20-JUN-2001; 2001WO-US019692.

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PA	(GETH)	GENENTECH INC.	
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PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
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Best Local Similarity 48.8%; Pred. No. 1.3e-26;			
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;			
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DB	1	MESGAYGAAGAGGSGFDLRRLFTQPVVARAVCLVFLVFCIYGGYSNAHESKQMYCV 60	
QY	61	YNRNPACSYGVAVGVLAFLTCLLLYLDVYFPQISVSKDKKAVLSDI 109	
DB	61	FNREDACRYGSAIGVLAFLASAFFLWVDAYFPQISNATDRKYLVIIGDL 109	
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DT	29-JAN-2004	(first entry)	
XX			
DE	Human secreted/transmembrane protein, PRO615.		
XX			
KW	Human; secreted protein; transmembrane protein; PRO; cytostatic;		
KW	ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnerary;		
KW	auditory; tumour growth; retinal disorder; sports-related joint problem;		
KW	articular cartilage defects; osteoarthritis; rheumatoid arthritis;		
KW	wound healing; hearing loss.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003203434-A1.		
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PD	30-OCT-2003.		
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PF	18-OCT-2001;	2001US-00145088.	
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PR	30-JUL-2001;	2001US-00918585.	
XX			
PA	(GETH)	GENENTECH INC.	
XX			
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;		
PI	Perrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;		
PI	Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;		
PI	Kljasin IJ, Kuo SS, Napier MA, Fan J, Paoni NF, Roy MA, Shelton DL;		
PI	Stewart TA, Tumas D, Williams PM, Wood WI;		
XX			
XX	WPI; 2003-875641/81.		
DR	N-PSDB; ADE35249.		

XX			
PT	New genes, and its encoded secreted and transmembrane polypeptides,		
PT	useful for treating e.g. lung or breast tumors, osteoarthritis,		
PT	rheumatoid arthritis, obesity, diabetes, hyperinsulinemia,		
PT	hypoinsulinemia or wounds.		
XX			
PS	Claim 12; SEQ ID NO 162; 462pp; English.		
XX			
CC	The invention relates to an isolated PRO polypeptide (secreted or		
CC	transmembrane protein) having at least 80% amino acid sequence identity		
CC	to an amino acid sequence chosen from 94 fully defined sequences as given		
CC	in the specification (including PRO lacking its associated signal		
CC	peptide, a PRO extracellular domain with or without its associated signal		
CC	peptide). Also included are nucleic acids encoding the PRO proteins		
CC	mentioned above, a vector comprising a PRO nucleic acid), a host cell		
CC	comprising the vector and producing PRO, a chimeric molecule comprising		
CC	PRO fused to a heterologous amino acid sequence, and an anti-PRO		
CC	antibody. PRO337 polypeptide is useful for detecting a PRO4993		
CC	polypeptide in a sample suspected of containing PRO4993 polypeptide.		
CC	Similarly, PRO4993 polypeptide is useful for detecting PRO337		
CC	polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting		
CC	PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting a		
CC	PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for detecting a		
CC	bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive		
CC	molecule is the toxin, radiolabel, or an antibody. The bioactive molecule		
CC	causes death of the cell. PRO337 polypeptide is useful for linking a		
CC	bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725,		
CC	PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule		
CC	to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is		
CC	useful for linking a bioactive molecule to a cell expressing PRO725,		
CC	PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337		
CC	polypeptide is useful for modulating at least one biological activity of		
CC	the cell expressing PRO337 polypeptide, where the cell is killed. PRO337		
CC	polypeptide or anti-PRO4993 polypeptide is useful for modulating the		
CC	biological activity of the cell expressing PRO4993 polypeptide; PRO725,		
CC	PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for		
CC	modulating the biological activity of the cell expressing PRO1559		
CC	polypeptide; and PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-		
CC	PRO739 polypeptide is useful for modulating the biological activity of		
CC	the cell expressing PRO725, PRO700 or PRO739 polypeptide. The		
CC	polypeptides are useful for inhibiting tumour growth, retinal disorders,		
CC	sports-related joint problems, articular cartilage defects,		
CC	osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in		
CC	mammals. The present sequence represents a PRO protein.		
XX			
SQ	Sequence 224 AA;		
Query Match 42.1%; Score 296; DB 7; Length 224;			
Best Local Similarity 48.6%; Pred. No. 1.3e-26;			
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;			
QY	1	MEGGAYGAGKAGGAFDPTLVROPHITLRVSWLFSIVVFGSIVNEGYNLSASEGEQFCI 60	
DB	1	MESGAYGAAGAGGSGFDLRRLFTQPVVARAVCLVFLVFCIYGGYSNAHESKQMYCV 60	
QY	61	YNRNPACSYGVAVGVLAFLTCLLLYLDVYFPQISVSKDKKAVLSDI 109	
DB	61	FNREDACRYGSAIGVLAFLASAFFLWVDAYFPQISNATDRKYLVIIGDL 109	
RESULT 50			
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ID	ADE16364	standard; protein; 224 AA.	
XX			
AC	ADE16364;		
XX			
DT	29-JAN-2004	(first entry)	
XX			
DE	Human secreted/transmembrane protein, PRO615.		
XX			
KW	Human; secreted protein; transmembrane protein; PRO; cytostatic;		
KW	ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnerary;		
KW	auditory; tumour growth; retinal disorder; sports-related joint problem;		

KW	articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW	wound healing; hearing loss.
XX	
OS	Homo sapiens.
XX	
PN	US2003203435-A1.
PP	
PD	30-OCT-2003.
XX	
PF	18-OCT-2001; 2001US-00145092.
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PR	30-APR-1998; 98US-0083742P.
PR	08-MAR-1999; 99WO-US005028.
PR	23-JUN-1999; 99US-014037P.
PR	25-AUG-1999; 99US-00380138.
PR	18-FEB-2000; 2000WO-US004341.
PR	30-JUL-2001; 2001US-00918585.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI	Perrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI	Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI	Kijavini IJ, Kuo SS, Napier WA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI	Stewart TA, Tumas D, Williams PW, Wood W;
XX	
XX	WPI; 2003-875642/81.
DR	N-PSDB; ADE16363.
XX	
PT	New genes, and its encoded secreted and transmembrane polypeptides,
PT	useful for treating e.g. lung or breast tumors, osteoarthritis,
PT	rheumatoid arthritis, obesity, diabetes, hyperinsulinemia,
PT	hypoinsulinemia or wounds.
XX	
PS	Claim 12; SEQ ID NO 162; 452pp; English.
XX	
CC	The invention relates to an isolated PRO polypeptide (secreted or
CC	transmembrane protein) having at least 80% amino acid sequence identity
CC	to an amino acid sequence chosen from 94 fully defined sequences as given
CC	in the specification (including PRO lacking its associated signal
CC	peptide, a PRO extracellular domain with or without its associated signal
CC	peptide). Also included are nucleic acids encoding the PRO proteins
CC	mentioned above, a vector comprising a PRO nucleic acid, a host cell
CC	comprising the vector and producing PRO, a chimeric molecule comprising
CC	PRO fused to a heterologous amino acid sequence, and an anti-PRO
CC	antibody. PRO337 polypeptide is useful for detecting a PRO4993
CC	polypeptide in a sample suspected of containing PRO4993 polypeptide.
CC	Similarly, PRO4993 polypeptide is useful for detecting PRO337
CC	polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
CC	PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
CC	PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
CC	bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive
CC	molecule is the toxin, radiolabel, or an antibody. The bioactive molecule
CC	causes death of the cell. PRO337 polypeptide is useful for linking a
CC	bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725,
CC	PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule
CC	to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is
CC	useful for linking a bioactive molecule to a cell expressing PRO725,
CC	PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337
CC	polypeptide is useful for modulating at least one biological activity of
CC	the cell expressing PRO337 polypeptide, where the cell is killed. PRO337
CC	polypeptide or anti-PRO4993 polypeptide is useful for modulating the
CC	biological activity of the cell expressing PRO4993 polypeptide; PRO725,
CC	PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for
CC	modulating the biological activity of the cell expressing PRO1559
CC	polypeptide; and PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-
CC	PRO739 polypeptide is useful for modulating the biological activity of
CC	the cell expressing PRO725, PRO700 or PRO739 polypeptide. The
CC	polypeptides are useful for inhibiting tumour growth, retinal disorders,
CC	sports-related joint problems, articular cartilage defects,
CC	osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in
CC	mammals. The present sequence represents a PRO protein.
XX	

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 42 Seconds
(without alignments)
234.611 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	296	42.1	224	2	US-08-700-637-2
5	291	41.4	56	4	US-09-621-976-4130
6	100	14.2	63	4	US-09-513-999C-4596
7	82	11.7	907	2	US-09-010-928B-4
8	78	11.1	253	4	US-09-248-796A-15975
9	73	10.4	407	2	US-08-776-585-3
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ALIGNMENTS

RESULT 1
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; Sequence 4379, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4379
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41..-1
; OTHER INFORMATION: score 4.3
; OTHER INFORMATION: seq RVVSWLFSIVVFG/SI
US-09-513-999C-4379

Query Match 82.1%; Score 577; DB 4; Length 112;
Best Local Similarity 99.1%; Pred. No. 1.5e-58;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY	61	YNRNPACSYGAVGVLAFLTCLLYLALDVFPQISSVKDKKAVLSDIGVS	112
DB	61	YNRNPACSYGAVGVLAFLTCLLYLALDVFPQISSVKDKKAVLSDIGVS	112

RESULT 2
US-09-949-016-6539
; Sequence 6539, Application US/09949016
; Patent No. 6812339

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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6539
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6539

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Best Local Similarity 99.1%; Pred. No. 4.1e-58;
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RESULT 3
US-08-700-637-3
; Sequence 3, Application US/08700637
; Patent No. 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; US-09-949-016-6539
```

```
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI 1072118
; US-08-700-637-3

Query Match      73.9%; Score 519.5; DB 2; Length 231;
Best Local Similarity 90.2%; Pred. No. 1.6e-51;
Matches 101; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY      1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSVLFSIVVFGSIIVNEGYLNSASEGEQFCI 60
Db      1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSVLFSIVVFGSIIVNEGYLNSASEGEFCI 57

QY      61 YNRNPACSYGAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVS 112
Db      58 YNRNPACSYGVTGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVS 109

RESULT 4
US-08-700-637-2
; Sequence 2, Application US/08700637
; Patent No. 5854413
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,637
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0065 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 224 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: COLNNOT05
; CLONE: 775426
; US-08-700-637-2

Query Match      42.1%; Score 296; DB 2; Length 224;
Best Local Similarity 48.6%; Pred. No. 7.1e-26;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY      1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSVLFSIVVFGSIIVNEGYLNSASEGEQFCI 60
Db      1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSVLFSIVVFGSIIVNEGYLNSASEGEQFCI 60

QY      61 YNRNPACSYGAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSIDIGVS 109
Db      61 FNRNEDACRYGSAIGVLAFLASAFVLVDAYFPQISNATDRKYLVIIGDL 109
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RESULT 5

US-09-621-976-4130
; Sequence 4130, Application US/09621976
; Patent No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S. J.Y.
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 4130

LENGTH: 56

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: -41...-1

US-09-621-976-4130

Query Match 41.4%; Score 291; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.3e-26;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHILRVVSWLFSIVVFGSIVNGLNSASEGE 56
|||||
DB 1 MEGGAYGAGKAGGAGDPYTLVRQPHILRVVSWLFSIVVFGSIVNGLNSASEGE 56
|||||

RESULT 6

US-09-513-999C-4596
; Sequence 4596, Application US/09513999C
; Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 4596

LENGTH: 63

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: -39...-1

OTHER INFORMATION: score 4.6

OTHER INFORMATION: seq AFLSCLAFVLDT/QE

FEATURE:

NAME/KEY: UNSURE

LOCATION: 19

OTHER INFORMATION: Xaa=Cys or Phe or Ile or Leu or Arg or Ser

US-09-513-999C-4596

Query Match 14.2%; Score 100; DB 4; Length 63;
Best Local Similarity 42.0%; Pred. No. 0.00043;
Matches 21; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 59 CIYNRNPNACSYGAVGVLAFLTCLLYLALDVYFPQISSVKORKKAVLSD 108
|||||
DB 8 CILNSNSVACSFVAGGAGFLSCLAFVLDTQETRIAGTRFKTAFQLLD 57
|||||

RESULT 7

US-09-010-928B-4
; Sequence 4, Application US/09010928B
; Patent No. 5994099

GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V

APPLICANT: Hayashi, Cheryl Y

TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA

TITLE OF INVENTION: CODING THEREFOR

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS: 29

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 8110 GATEHOUSE RD. SUITE 500E

CITY: FALLS CHURCH

STATE: VIRGINIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/010,928B

FILING DATE: 22-JAN-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M

REGISTRATION NUMBER: 28977

REFERENCE/DOCKET NUMBER: 1447-109P

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 907 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-010-928B-4

Query Match 11.7%; Score 82; DB 2; Length 907;
Best Local Similarity 32.9%; Pred. No. 1.7;
Matches 28; Conservative 14; Mismatches 27; Indels 16; Gaps 5;

QY 3 GGAYGAGKAGGAGDPYTLVRQPHILRVVSWL----FSIVVFGSIVNGLNSASEGEQF 58
|||||
DB 805 GGAYGFGSPGAYVPSS--RVPDMVNGINSAMQSGGFNYQMFGNM-----LSQVSSGSGT 857
|||||

QY 59 CIYNRNPNACSYGAVGVLAFLTCL 83
|
DB 858 C-----NPNNVNV-LMDALLAALHCL 877
|

RESULT 8

US-09-248-796A-15975
; Sequence 15975, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

OTHER INFORMATION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15975

LENGTH: 253

TYPE: PRT

ORGANISM: Candida albicans


```

; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1109
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11109

Query Match      10.2%; Score 72; DB 4; Length 714;
Best Local Similarity 25.2%; Pred. No. 17;
Matches 31; Conservative 19; Mismatches 49; Indels 24; Gaps 5

Qy 9 GKAGGAFDPYTLVRQP-----H-TIRVVSWLFSIVVFGSIVNEGVLNSASEGEQ--- 57
Db 6 GSHAGPAPAAEAERRPACRERYHLVSRPVSIFIVHP-----NRAQEEVQRVF 56

Qy 58 ---FCIYNRNPACSYGAVGVLAFPLTCLLYLALDVYFPQISSVKDRKAVLSDIGV-SG 113
Db 57 DRFFHLHLRLFPQAAGVADARLTMLNLVALSVVIAAFHFTFEGAREREAIAQRTMFEAG 116

Qy 114 EPH 116
Db 117 EQH 119

RESULT 12
US-09-659-519-4
; Sequence 4, Application US/09659519
; Patent No. 6783973
; GENERAL INFORMATION:
; APPLICANT: Grandy, David K
; APPLICANT: Bunzow, James R
; TITLE OF INVENTION: Mammalian Catecholamine Receptor Genes and Uses
; FILE REFERENCE: Catecholamine receptor genes
; CURRENT APPLICATION NUMBER: US/09/659,519
; CURRENT FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-659-519-4

Query Match      10.2%; Score 71.5; DB 4; Length 332;
Best Local Similarity 25.7%; Pred. No. 7.1;
Matches 26; Conservative 19; Mismatches 37; Indels 19; Gaps 6

Qy 27 ILRVVSW-LFSIVVFGSIVNEGVLNSASE--GEQFCIYNRNPAC--SYGVAVGVLAEL 80
Db 141 VMILISWSLPAVFAFGMIFLELNLEGVEEQYHNVFCL-----RGCLFFFSKVSGVLAEM 195

Qy 81 T-----CLLYLALDVYFPQISSVKDRKAVLSDIGVSGE 114
Db 196 TSFYIPGWSVLMFVYIEIPIAKQARSINRANL-QVGLEGE 235

RESULT 13
US-07-783-602C-1
; Sequence 1, Application US/07783602C
; Patent No. 5418160
; GENERAL INFORMATION:
; APPLICANT: J. Craig Venter et al
; TITLE OF INVENTION: A FAT CELL SPECIFIC a-ADRENERGIC
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza

```

```

; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40, 489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5743:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...525
; SEQUENCE DESCRIPTION: SEQ ID NO: 5743:
US-09-107-532A-5743

Query Match 10.2%; Score 71.5; DB 4; Length 525;
Best Local Similarity 23.1%; Pred. No. 13;
Matches 33; Conservative 19; Mismatches 34; Indels 57; Gaps 7;

Qy 10 KAGAFDPYTLVRQPHITLRVSWLFSIVVFGSIVNEG---YLSASSEGQFCIYNR--- 63
Db 235 KAGAFQSITLV-----CKLIP-LFVIVIFGLPRQGVDFQLFPQAGENLSFFSALGA 287
Qy 64 -----NPNACSYGVAVGVLAFLTCLLYALDVPFQI 95
Db 288 GLLATMFAYDGIHWGNISGELKPKADLPKALISLGI-IGIM-----IVYLLVNAVFLRT 341
Qy 96 SSVKDRKKAVLSDIGVSGEPHPA 118
Db 342 ASID-----GVAGNSNAA 354

RESULT 15
US-09-540-236-2307
; Sequence 2307, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2307
; LENGTH: 488
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2307

Query Match 10.1%; Score 71; DB 4; Length 488;
Best Local Similarity 24.6%; Pred. No. 14;
Matches 28; Conservative 12; Mismatches 28; Indels 46; Gaps 7;

Qy 31 VSWLFSI-VVFGSIVNEGYSASGEQFCIYNRNPNACSYGVAVGVLAFLTCLLYALD 89
Db 208 MTWIFILVFTVQTNAGYMR-----EHMCVY-----ICPYG----- 239
Qy 90 VYFFPOISSVK-DRKXAVLSDIGVSGEPH-----PAG-----TPCTESTEGCP 130
Db 240 ----RFQSVMFMDKTLIVSYDYERGEPRGARKDOTTAGYGDVDCVTCVQVCP 289

RESULT 16
US-07-745-206A-2

```

STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-49

Sequence 51, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
APPLICATION NUMBER: 07/745,206
FILING DATE: 15-AUG-1991
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 2161 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-51

Query Match 10.0%; Score 70; DB 1; Length 2161;
Best Local Similarity 25.5%; Pred. No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;
QY 2 EGGAYGAGKAGGAFDPYTL-----VRQPHILRVVSWLFSIVFGSIYNEGYLNSASEGEQ 57
Db 222 EGGNHSSKSGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263
QY 58 FCYINRNPNACSYGVAVGVLAFTCLLYLALDVYFP-----QISSVKDRKAVLSD 108
Db 264 -----IIKAMVPLLIHALLVLFVIIIVAIIGLELFIQGMHKTCPFAD 305
QY 109 IGVSGEHPHACTPC-----TESTEGCGPG 132
Db 306 SDVAEDPA--PCAFSGNGRQCTANGTECRSGWGP 340

RESULT 18
US-08-455-543A-51

```
Db      222 EGNHSSGKGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263
Qy      58 FCINYRNPACSYGVAVGVLAFTCLLYLALDYFFP-----QISSVKDRKKAVLSD 108
Db      264 -----IKAMVPLHLIALLVFVIIIVAIIGLELFLFGKVKHKTCTCFAD 305
Qy      109 IGVSGEPHPAGTPC-----TESTGCPGP 132
Db      306 SDIVAEEDPA--PCAFSGNGRQCTANGTECRSGWVGP 340

RESULT 19
US-08-223-305C-49
; Sequence 49, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; FILING DATE: April 4, 1994
; APPLICATION NUMBER: US/08/223,305C
; PRIOR APPLICATION DATA:
; FILING DATE: April 10, 1992
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 52516 (P519739)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0899
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-223-305C-49
Query Match 10.0%; Score 70; DB 2; Length 2161;
Best Local Similarity 25.5%; Pred No. 1.3e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;
Qy      2 EGGAYGAGKAGGAFDPYTL---VRQPHTILRVVSWLFSIVVFGSIVNVEGYLNSASEGQ 57
Db      222 EGNHSSGKGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263
Qy      58 FCINYRNPACSYGVAVGVLAFTCLLYLALDYFFP-----QISSVKDRKKAVLSD 108
Db      264 -----IKAMVPLHLIALLVFVIIIVAIIGLELFLFGKVKHKTCTCFAD 305
Qy      109 IGVSGEPHPAGTPC-----TESTGCPGP 132
Db      306 SDIVAEEDPA--PCAFSGNGRQCTANGTECRSGWVGP 340

RESULT 20
US-08-223-305C-51
; Sequence 51, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
```


ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,901
FILING DATE: 19920720
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-324 (WSU)
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: AMINO ACID
MOLECULE TYPE: protein
US-07-916-901-6

Query Match 9.9%; Score 69.5; DB 1; Length 400;
Best Local Similarity 25.3%; Pred. No. 15;
Matches 38; Conservative 20; Mismatches 51; Indels 41; Gaps 9;

QY 14 AFDPYTLVRQPHILR-----VSWLFSIVV-FGSIVNEGYNLSASEGEQF 58
DB 129 AVDRYLAVTNP---LRYGTLVTKRRARAAVLVWIVSATVSPAPIMSQWVRVGADAEAGE 185

QY 59 CIYNRNPNACS-----YGVAVGVLAFLTCLLYLALDVTFFPQISSVKDRKKAIVLSDIG-- 110
DB 186 C-HSNPRCCSPASNMPYALLSSVSFYLPLLVN-LFVYARVFWAKRQRLRLRELGRF 242

QY 111 -----VSGEPHFA--GTPCTESTEGCP 130
DB 243 PPEESPRSPRSFSPATVGTGTP--TASDGV 270

RESULT 27
US-08-351-473B-4
Sequence 4, Application US/08351473B
Patent No. 5656440
GENERAL INFORMATION:
APPLICANT: LENZEN, GERLINDA
APPLICANT: KAPOOR, ARCHANA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
TITLE OF INVENTION: BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
FILING DATE: 21-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6639-001-0X PCT
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-351-473B-4

Query Match 9.9%; Score 69.5; DB 1; Length 400;
Best Local Similarity 25.3%; Pred. No. 15;
Matches 38; Conservative 20; Mismatches 51; Indels 41; Gaps 9;

QY 14 AFDPYTLVRQPHILR-----VSWLFSIVV-FGSIVNEGYNLSASEGEQF 58
DB 129 AVDRYLAVTNP---LRYGTLVTKRRARAAVLVWIVSATVSPAPIMSQWVRVGADAEAGE 185

QY 59 CIYNRNPNACS-----YGVAVGVLAFLTCLLYLALDVTFFPQISSVKDRKKAIVLSDIG-- 110
DB 186 C-HSNPRCCSPASNMPYALLSSVSFYLPLLVN-LFVYARVFWAKRQRLRLRELGRF 242

QY 111 -----VSGEPHFA--GTPCTESTEGCP 130
DB 243 PPEESPRSPRSFSPATVGTGTP--TASDGV 270

RESULT 28
PCT-US91-01726-3
Sequence 3, Application PC/TUS9101726
GENERAL INFORMATION:
APPLICANT: Brown, Malcolm R
APPLICANT: Saxena, Inder M
APPLICANT: Lin, Fong C
TITLE OF INVENTION: Recombinant Cellulose Synthase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David L. Parker
STREET: 600 Congress Avenue Suite 2300
CITY: Austin
STATE: Texas
COUNTRY: United States
ZIP: 78701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01726
FILING DATE: 19910314
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 494093
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parker Mr. David L
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 809 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear

PCT-US91-01726-3

[illegible]

```

RESULT 29
US-09-227-357-510
; Sequence 510, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 510
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-510

```

Query Match	9.8%;	Score 69;	DB 3;	Length 18;
Best Local Similarity	72.2%;	Pred. No. 0.3;		
Matches 13;	Conservative	2;	Mismatches 3;	Indels 0;
				Gaps 0;

```

RESULT 30
US-09-252-991A-32320
; Sequence 32320, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND
; TITLE OF INVENTION: AERUGINOSA FOR DIA
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,9
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,78
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,19
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32320
; LENGTH: 197
; TYPE: PR
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32320

```

```

Query Match      9.7%; Score 68; DB 4; Length 197;
Best Local Similarity 25.5%; Pred. No. 9.1;
Matches 25; Conservative 7; Mismatches 36; Indels 30; Gaps 3;

QY      63  RNPNACSYGVAVGVLAFLTCLLYALDLYVFPQISVKD----- 100
Db      1  RMRPCGVGLVEGMPDGGAAAFVSVAVFVYNS--KDNLYCFAGSLACKRAAPGRSR 59

QY     101  ----RKKAVLSDTGVSGEHPHAG---TPCTESTEGCGPG 131
Db     60  SDPHRTKARGGVVSAAGRPQPMGRLLTHVLDSAHGCGPG 97

```

RESULT 31
US-09-107-532A-6471
; Sequence 6471, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...319
; SEQUENCE DESCRIPTION: SEQ ID NO: 6471:
US-09-107-532A-6471

Query Match 9.7%; Score 68; DB 4; Length 319;
Best Local Similarity 34.2%; Pred. No. 17;
Matches 27; Conservative 10; Mismatches 26; Indels 16; Gaps 4;
Qy 52 ASEGEQCIYNRPNACSY-----GVAVGLAPLTCLLYALDVPVQISSV-----KDR 101
Db 38 ASSEGTITMAEN-VPSGCFYMGKSVTNAELRAAGADILFNALDLPNFIQISGVPLTKEN 96
Qy 102 -----KKAVLSDIGVSGEP 115
Db 97 PIWIKKALGRAIGNLEP 115

RESULT 32
US-09-328-352-5497
; Sequence 5497, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5497
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5497

Query Match 9.7%; Score 68; DB 4; Length 462;
Best Local Similarity 22.2%; Pred. No. 28;
Matches 41; Conservative 22; Mismatches 48; Indels 74; Gaps 10;
Qy 3 GGAYGAG-----KAG-GAFDPYTLVRQPHITLRVV-----SW-33
Db 162 GGEYGASATYLSMAEKDRRFFSFQYVYTLIAGQITALCVLLILQMLITEQLHDGWR 221
Qy 34 -----LFSIVP-----GSIVNEGVLNSASGEQ-----FCIYNRPN-----ACSYGVAV 74
Db 222 VPFFIGALLAIVVFRIRRGLELTQSGFKNAQAETDQPKSGMFALFKHYPKAEFTVLELTAG 281
Qy 75 GVLAFLTCLLY-----LALDVPF-----LQISSVKDR--KKAVLSD 108
Db 282 GTLAFAYTYTYTLQKYLNTSGFTKPEATOITLALFIFMCLQPLAGLSDRIGRKPIMIA 341
Qy 109 IGVSQ 113
Db 342 FGVG 346

RESULT 33
US-09-949-016-11276
; Sequence 11276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11276
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11276

Query Match 9.7%; Score 68; DB 4; Length 689;
Best Local Similarity 35.7%; Pred. No. 47;
Matches 15; Conservative 5; Mismatches 20; Indels 2; Gaps 1;
Qy 93 PQISSVKDR--KKAVLSDIGVSGEPHPAGTPCTTESTGCGP 132
Db 186 PGLQGVKHAGKRGILGDPGHQKPGKGDVGASGQGIQGP 227

RESULT 34
US-09-134-000C-5534
; Sequence 5534, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

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; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5534
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-5534

Query Match          9.7%; Score 68; DB 4; Length 706;
Best Local Similarity 24.3%; Pred. No. 49;
Matches 27; Conservative 19; Mismatches 39; Indels 26; Gaps 4;

QY 13 GAFDPYTLVRQPHITLRV---SWLFSIVVFGSIVNVEGYLNSASEGEQFCIYNRNPNACS 69
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 484 GSNDPVALRRQTYGVIRIIEKGTWTPPLQLQTEVDEAV-----NQDVEK 528

QY 70 YGVAVG-----VLAFITC---LLYALDVYFPPOISSVKORKKAVLSDIGVS 112
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 529 YGYLLNEGOAEVVEFKARLQLMTKNVRHDIIDAVVSAEQADLSKLFAS 579

RESULT 35
US-09-949-016-11448
; Sequence 11448, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11448
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11448

Query Match          9.6%; Score 67.5; DB 4; Length 436;
Best Local Similarity 22.6%; Pred. No. 29;
Matches 33; Conservative 20; Mismatches 54; Indels 39; Gaps 6;

QY 11 AGGAFDPYTLVRQPHITLRVSVWLSFIVVFGS-----IVNEGYLN-----SASEG 55
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 187 SGSAGSFILCVGGLISQALSWPFIYFGTGCVCCLLWFTVIYDDPMHHCISVREK 246

QY 56 EQFCIYNRNPNACSYGVAVGVLAFLTCL-----LYLA-----LDVYFPQISS 97
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 247 EHI-LSSLAQOPSPGPAVPIKAWTCLPLWAIPLGFFSHFWLCTILTYLPTIYISTLLH 305

QY 98 VKDRKXAVLSDIGVSGEPHAGTPTCT 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 VNIRDSGLVSSL-----PFIATAASCT 326

RESULT 36
US-08-724-394A-10
; Sequence 10, Application US/08724394A
; Patent No. 587237
; GENERAL INFORMATION:

```

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; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Teuchihaashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 470 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..470
; OTHER INFORMATION: /note= "NPT3"
; US-08-724-394A-10

Query Match          9.6%; Score 67.5; DB 2; Length 470;
Best Local Similarity 22.6%; Pred. No. 33;
Matches 33; Conservative 20; Mismatches 54; Indels 39; Gaps 6;

QY 11 AGGAFDPYTLVRQPHITLRVSVWLSFIVVFGS-----IVNEGYLN-----SASEG 55
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 187 SGSAGSFILCVGGLISQALSWPFIYFGTGCVCCLLWFTVIYDDPMHHCISVREK 246

QY 56 EQFCIYNRNPNACSYGVAVGVLAFLTCL-----LYLA-----LDVYFPQISS 97
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 247 EHI-LSSLAQOPSPGPAVPIKAWTCLPLWAIPLGFFSHFWLCTILTYLPTIYISTLLH 305

QY 98 VKDRKXAVLSDIGVSGEPHAGTPTCT 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 VNIRDSGLVSSL-----PFIATAASCT 326

RESULT 37
US-09-538-092-354
; Sequence 354, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092

```

6555339-Endogenous, Constitutively Activated Human G Protein

; SEQ ID NO 306
; LENGTH: 907
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-306

Query Match 9.5%; Score 67; DB 4; Length 907;
Best Local Similarity 24.8%; Pred. No. 88;
Matches 30; Conservative 15; Mismatches 52; Indels 24; Gaps 6;

QY 14 APDPYTLVRQPHILRVWSWLFISIVVFGSIVN--EGYLSASGEQFCIYNR---NPNAC 68

DB 110 AIDP---PRSPLFYRIVIVWSLTISYTSFWGVDFQFNLDQGRHFCIFNAIIFLGDAI 166

QY 69 SYGVAV-----GVLAFLTCLLYLALDVYFPQISSVKDKKAVLSDIGV---SGEPH 116

DB 167 GSGIIASLVHTIGIQLILFTAAVLVT----FPVIVYVSKSLKSLSDDHDLFIDTGHPP 222

QY 117 P 117

DB 223 P 223

RESULT 42

US-09-438-185A-295

; Sequence 295, Application US/09438185A

; Patent No. 6822071

; GENERAL INFORMATION:

; APPLICANT: Stephens, Richard

; APPLICANT: Mitchell, Wayne

; APPLICANT: Kalman, Sue

; APPLICANT: Davis, Ronald

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence

; FILE REFERENCE: 018941-000411US

; CURRENT APPLICATION NUMBER: US/09/438,185A

; PRIOR FILING DATE: 2002-03-13

; PRIOR APPLICATION NUMBER: US 60/108,279

; PRIOR FILING DATE: 1998-11-12

; PRIOR APPLICATION NUMBER: US 60/128,606

; PRIOR FILING DATE: 1999-04-08

; NUMBER OF SEQ ID NOS: 1074

; SOFTWARE: Fast-SEQ for Windows Version 3.0

; SEQ ID NO 295

; LENGTH: 928

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; FEATURE:

; OTHER INFORMATION: CPn0293

US-09-438-185A-295

Query Match 9.5%; Score 67; DB 4; Length 928;
Best Local Similarity 24.8%; Pred. No. 91;
Matches 30; Conservative 15; Mismatches 52; Indels 24; Gaps 6;

QY 14 APDPYTLVRQPHILRVWSWLFISIVVFGSIVN--EGYLSASGEQFCIYNR---NPNAC 68

DB 110 AIDP---PRSPLFYRIVIVWSLTISYTSFWGVDFQFNLDQGRHFCIFNAIIFLGDAI 166

QY 69 SYGVAV-----GVLAFLTCLLYLALDVYFPQISSVKDKKAVLSDIGV---SGEPH 116

DB 167 GSGIIASLVHTIGIQLILFTAAVLVT----FPVIVYVSKSLKSLSDDHDLFIDTGHPP 222

QY 117 P 117

DB 223 P 223

RESULT 43

US-10-012-762-20

; Sequence 20, Application US/10012762

; Patent No. 6635438

; GENERAL INFORMATION:

; APPLICANT: KAWASAKI, GLENN
; APPLICANT: WEBB, HEATHER K.
; APPLICANT: OWENS, JEFFREY
; APPLICANT: LIEDTKE, RAYMOND
; APPLICANT: FOREST, DOREEN
; APPLICANT: LEGAZ, MARK
; APPLICANT: LAWSON, SOBOMABO
; TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE
; FILE REFERENCE: 30865
; CURRENT APPLICATION NUMBER: US/10/012,762
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: 60/163,126
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: 09/704,036
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/203,349
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1252
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-012-762-20

Query Match 9.5%; Score 67; DB 4; Length 1252;
Best Local Similarity 34.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 10; Mismatches 20; Indels 2; Gaps 2;

QY 84 LYLALDVYFPQISSVKDR-KKAVLSDIGVSGEPHPAGTPTCTESTGCPG 131

DB 277 IYAKLELYNPG-GSIKDRIAKSMVEAEASGRHFSRSTLIPTSGNTG 324

RESULT 44

US-09-704-036B-20

; Sequence 20, Application US/09704036B

; Patent No. 6664073

; GENERAL INFORMATION:

; APPLICANT: KAWASAKI, GLENN

; APPLICANT: WEBB, HEATHER

; APPLICANT: OWENS, JEFFREY

; APPLICANT: LIEDTKE, RAYMOND

; APPLICANT: FOREST, DOREEN

; APPLICANT: LEGAZ, MARK

; APPLICANT: LAWSON, SOBOMABO

; TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE

; FILE REFERENCE: 30865

; CURRENT APPLICATION NUMBER: US/09/704,036B

; CURRENT FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: 60/163,126

; PRIOR FILING DATE: 1999-11-02

; PRIOR APPLICATION NUMBER: 09/704,036

; PRIOR FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: 60/203,349

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 20

; LENGTH: 1252

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

US-09-704-036B-20

Query Match 9.5%; Score 67; DB 4; Length 1252;
Best Local Similarity 34.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 10; Mismatches 20; Indels 2; Gaps 2;

QY 84 LYLALDVYFPQISSVKDR-KKAVLSDIGVSGEPHPAGTPTCTESTGCPG 131

DB 277 IYAKLELYNPG-GSIKDRIAKSMVEAEASGRHFSRSTLIPTSGNTG 324

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RESULT 45
US-09-519-232-74
; Sequence 74, Application US/09519232
; Patent No. 6528702
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weiss, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTF2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 74
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-519-232-74

Query Match          9.5%; Score 66.5; DB 4; Length 369;
Best Local Similarity 24.2%; Pred. No. 31;
Matches 30; Conservative 19; Mismatches 42; Indels 33; Gaps 5;

QY 5 AYGAGKAGGAFDPTLVROPHITLVRVSMFLFSIVWFGSIVNEGYLNSASGEQFCI----60
Db 32 AYGSGTSGSYEIIISLKSNNLEQLLSDSSDFTDAEIVVEG-----VSLGVHRCILAAR 87
QY 61 -----YNNRPNACS-----YGVAVGLVFLTCLLYL---ALDVPFPQIS 96
Db 88 SKFFQDLFRKEKSCGKEGPRYSMTDILPYG-KVGVEAFVTLSYLSKLGKHPPEVS 146
QY 97 SVKD 100
Db 147 TCMD 150

RESULT 46
US-09-441-411-8
; Sequence 8, Application US/09441411
; Patent No. 6734172
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-441-411-8

Query Match          9.5%; Score 66.5; DB 4; Length 378;
Best Local Similarity 23.0%; Pred. No. 32;
Matches 29; Conservative 22; Mismatches 44; Indels 31; Gaps 7;

QY 4 GAY---GAGKAGGA--FDPTLVROPHITLVRVSMFLS-----HTILRVVSWLFS---IVV-----FG 41
Db 133 GSYSGIGAGMTAAIGDYRVNVTKPMNRNMTFTKAVIMNIIWLYCTPWVVLPTQFWD 192
QY 42 SIVNEGYLNSASGEQFCIYNNRPNACSIVAVGVLAFLT---CLLYLALDVPFPQISSVK 99
Db 193 RFVPEGYLTS-----CSFDYLSDNFTLRFVGTIFPFVSPVCTLMILYIYSIOVGHV 245
QY 100 DRKAV 105
; :|||:

RESULT 47
US-09-489-039A-9365
; Sequence 9365, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9365
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9365

Query Match          9.4%; Score 66; DB 4; Length 237;
Best Local Similarity 23.4%; Pred. No. 20;
Matches 25; Conservative 20; Mismatches 32; Indels 30; Gaps 4;

QY 13 GAFDPVTLV--RQPHITLVRVSWLFSI-----VVFGSIVNEGYL 49
Db 107 GFYSLSLVFRQHQWKSRLVALIFAIAWIVLGLSFVNVPLNGMSSLAIFGLFLVLGGI 166
QY 50 NSAGEGEQFCIYNNRPNACSIVAVGVLAFLTCLLYLALDVPFPQIS 96
Db 167 SRVNGCQ----TRKQSGAGWNIFIGLLDLLIACLWLAWN---PQGS 206

RESULT 48
US-09-090-567-2
; Sequence 2, Application US/09090567
; Patent No. 5989549
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Robert
; APPLICANT: Lgar, Bruno
; APPLICANT: Lgar, Christine
; APPLICANT: Gaudreault, Christian
; TITLE OF INVENTION: Acrosomal Sperm Protein And
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swabey Ogilvy Renault
; STREET: 1600 - 1981 McGill College
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/090,567
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Kevin P
; REGISTRATION NUMBER: 26,674
; REFERENCE/DOCKET NUMBER: 13045-2"US" FC/CC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514-845-7126
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/ TELEFAX: 514-288-8389
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 244 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/
US-09-090-567-2
    Query Match          9.4%; Score 66; DB 2; Length 244;
    Best Local Similarity 25.2%; Pred. No. 20;
    Matches 26; Conservative 16; Mismatches 43; Indels 18; Gaps 4;

QY 26 TLIRVSVWLFSLVFGSIWEGYNSAGEQFCIYNRPNACSYGVAVGVLAFLTCLLY 85
Db 110 SVLQV-----SQVAKGMINRGVAGSIVNLSVVAVVTFPGLATYSSTKGAITMLTKAMA 164

QY 86 LALDVYFPOISSVKDRKKAVALSDIG--VSSEP-----HP 117
Db 165 MELGPYKIRVNSV--NPTVLTDMGKKVSADPEFAKKLKERHP 205

RESULT 49
US-08-118-270-10
/ Sequence 10, Application US/08118270
/ Patent No. 5508384
/ GENERAL INFORMATION:
/ APPLICANT: Murphy, Randall B.
/ ATTORNEY/AGENT INFORMATION:
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/118,270
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY-2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 317 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-118-270-10
    Query Match          9.4%; Score 66; DB 1; Length 317;
    Best Local Similarity 22.5%; Pred. No. 29;
    Matches 27; Conservative 24; Mismatches 43; Indels 26; Gaps 5;

QY 26 TLIRVSVWLFSLVFGSIWEGYNSAGEQFCIYNRPNACSYGVAVGVLAFLTCLLY 85
Db 110 SVLQV-----SQVAKGMINRGVAGSIVNLSVVAVVTFPGLATYSSTKGAITMLTKAMA 164

QY 86 LALDVYFPOISSVKDRKKAVALSDIG--VSSEP-----HP 117
Db 165 MELGPYKIRVNSV--NPTVLTDMGKKVSADPEFAKKLKERHP 205

RESULT 49
US-08-118-270-10
/ Sequence 10, Application US/08118270
/ Patent No. 5508384
/ GENERAL INFORMATION:
/ APPLICANT: Murphy, Randall B.
/ ATTORNEY/AGENT INFORMATION:
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/118,270
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY-2A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 317 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-118-270-10
    Query Match          9.4%; Score 66; DB 1; Length 317;
    Best Local Similarity 22.5%; Pred. No. 29;
    Matches 27; Conservative 24; Mismatches 43; Indels 26; Gaps 5;
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QY 14 APDPYTLVRQPH-----ILRVVSWLFSLVFGSIWEGYNSASEG 55
Db 85 SFDYFCVTKPLTYPVKRTTKMAGNMIAAAVLSFILWAPAILFWQFVG---VRTVEDG 141
QY 56 EQFCIYNRPNACSYGVAVGVLAFLTCLLYLALDVYFPOISS---VKDRKKAVALSDIGVS 112
Db 142 ECVIOFFSNP-AVTFGTAIAAF-YLPVIMIVLYWHISRAKSRIRKKOKKEPVANQDPVS 199

RESULT 50
PCT-US93-08528-10
/ Sequence 10, Application PC/TUS9308528
/ GENERAL INFORMATION:
/ APPLICANT: New York University
/ TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
/ NUMBER OF SEQUENCES: 348
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/08528
/ FILING DATE: 09-SEP-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/943,236
/ FILING DATE: 10-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Townsend, Kevin G.
/ REGISTRATION NUMBER: 34,033
/ REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ TELEX: 248633
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 317 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
PCT-US93-08528-10
    Query Match          9.4%; Score 66; DB 5; Length 317;
    Best Local Similarity 22.5%; Pred. No. 29;
    Matches 27; Conservative 24; Mismatches 43; Indels 26; Gaps 5;

QY 14 APDPYTLVRQPH-----ILRVVSWLFSLVFGSIWEGYNSASEG 55
Db 85 SFDYFCVTKPLTYPVKRTTKMAGNMIAAAVLSFILWAPAILFWQFVG---VRTVEDG 141
QY 56 EQFCIYNRPNACSYGVAVGVLAFLTCLLYLALDVYFPOISS---VKDRKKAVALSDIGVS 112
Db 142 ECVIOFFSNP-AVTFGTAIAAF-YLPVIMIVLYWHISRAKSRIRKKOKKEPVANQDPVS 199

Search completed: August 11, 2005, 08:24:36
Job time : 43 secs
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:54 ; Search time 60 Seconds
(without alignments)
859.837 Million cell updates/sec

Title: US-10-643-836-297
Perfect score: 703
Sequence: 1 MEGGAYGAGKAGAFDPYTL.....GEPHPAGTCTESTGCGP 132

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1755696

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 50 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	703	100.0	132	10	US-09-876-997-297
3	703	100.0	132	17	US-10-643-836-297
4	296	42.1	224	9	US-09-788-295A-162
5	296	42.1	224	9	US-09-788-697-162
6	296	42.1	224	9	US-09-788-192A-162
7	296	42.1	224	9	US-09-999-832A-162
8	296	42.1	224	10	US-09-978-189-162
9	296	42.1	224	10	US-09-978-608A-162
10	296	42.1	224	10	US-09-978-585A-162
11	296	42.1	224	10	US-09-978-191A-162

12	296	42.1	224	10	US-09-978-403A-162
13	296	42.1	224	10	US-09-978-564A-162
14	296	42.1	224	10	US-09-989-833A-162
15	296	42.1	224	10	US-09-981-915A-162
16	296	42.1	224	10	US-09-978-824-162
17	296	42.1	224	10	US-09-918-585A-162
18	296	42.1	224	10	US-09-999-834A-162
19	296	42.1	224	10	US-09-978-423A-162
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21	296	42.1	224	10	US-09-999-830A-162
22	296	42.1	224	10	US-09-978-757A-162
23	296	42.1	224	10	US-09-978-187B-162
24	296	42.1	224	10	US-09-978-643A-162
25	296	42.1	224	10	US-09-978-375A-162
26	296	42.1	224	10	US-09-978-298A-162
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28	296	42.1	224	10	US-09-978-681A-162
29	296	42.1	224	10	US-09-978-194A-162
30	296	42.1	224	10	US-09-999-829A-162
31	296	42.1	224	10	US-09-978-299A-162
32	296	42.1	224	10	US-09-978-544A-162
33	296	42.1	224	10	US-09-978-665A-162
34	296	42.1	224	10	US-09-978-802A-162
35	296	42.1	224	11	US-09-999-831A-162
36	296	42.1	224	12	US-09-978-824-162
37	296	42.1	224	14	US-10-017-081A-162
38	296	42.1	224	14	US-10-167-749-162
39	296	42.1	224	14	US-10-013-921A-162
40	296	42.1	224	14	US-10-016-177A-162
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42	296	42.1	224	14	US-10-143-031A-162
43	296	42.1	224	14	US-10-143-030A-162
44	296	42.1	224	14	US-10-002-967A-162
45	296	42.1	224	14	US-10-017-083A-162
46	296	42.1	224	14	US-10-145-128A-162
47	296	42.1	224	14	US-10-017-191A-162
48	296	42.1	224	14	US-10-143-028A-162
49	296	42.1	224	14	US-10-143-029A-162
50	296	42.1	224	14	US-10-143-029A-162

ALIGNMENTS

RESULT 1
US-09-731-872-297
; Sequence 297, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78.053.REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 297
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41..-1
US-09-731-872-297

Query Match 100.0%; Score 703; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.3e-73;

1	PRIOR FILING DATE: 1998-04-09
2	PRIOR APPLICATION NUMBER: 60/081955
3	PRIOR FILING DATE: 1998-04-15
4	PRIOR APPLICATION NUMBER: 60/081817
5	PRIOR FILING DATE: 1998-04-15
6	PRIOR APPLICATION NUMBER: 60/081819
7	PRIOR FILING DATE: 1998-04-15
8	PRIOR APPLICATION NUMBER: 60/081952
9	PRIOR FILING DATE: 1998-04-15
10	PRIOR APPLICATION NUMBER: 60/081838
11	PRIOR FILING DATE: 1998-04-15
12	PRIOR APPLICATION NUMBER: 60/082568
13	PRIOR FILING DATE: 1998-04-21
14	PRIOR APPLICATION NUMBER: 60/082569
15	PRIOR FILING DATE: 1998-04-21
16	PRIOR APPLICATION NUMBER: 60/082704
17	PRIOR FILING DATE: 1998-04-22
18	PRIOR APPLICATION NUMBER: 60/082804
19	PRIOR FILING DATE: 1998-04-22
20	PRIOR APPLICATION NUMBER: 60/082700
21	PRIOR FILING DATE: 1998-04-22
22	PRIOR APPLICATION NUMBER: 60/082797
23	PRIOR FILING DATE: 1998-04-22
24	PRIOR APPLICATION NUMBER: 60/082796
25	PRIOR FILING DATE: 1998-04-23
26	PRIOR APPLICATION NUMBER: 60/083336
27	PRIOR FILING DATE: 1998-04-27
28	PRIOR APPLICATION NUMBER: 60/083322
29	PRIOR FILING DATE: 1998-04-28
30	PRIOR APPLICATION NUMBER: 60/083392
31	PRIOR FILING DATE: 1998-04-29
32	PRIOR APPLICATION NUMBER: 60/083495
33	PRIOR FILING DATE: 1998-04-29
34	PRIOR APPLICATION NUMBER: 60/083496
35	PRIOR FILING DATE: 1998-04-29
36	PRIOR APPLICATION NUMBER: 60/083499
37	PRIOR FILING DATE: 1998-04-29
38	PRIOR APPLICATION NUMBER: 60/083545
39	PRIOR FILING DATE: 1998-04-29
40	PRIOR APPLICATION NUMBER: 60/083554
41	PRIOR FILING DATE: 1998-04-29
42	PRIOR APPLICATION NUMBER: 60/083558
43	PRIOR FILING DATE: 1998-04-29
44	PRIOR APPLICATION NUMBER: 60/083559
45	PRIOR FILING DATE: 1998-04-29
46	PRIOR APPLICATION NUMBER: 60/083500
47	PRIOR FILING DATE: 1998-04-29
48	PRIOR APPLICATION NUMBER: 60/083742
49	PRIOR FILING DATE: 1998-04-30
50	PRIOR APPLICATION NUMBER: 60/084366
51	PRIOR FILING DATE: 1998-05-05
52	PRIOR APPLICATION NUMBER: 60/084414
53	PRIOR FILING DATE: 1998-05-06
54	PRIOR APPLICATION NUMBER: 60/084441
55	PRIOR FILING DATE: 1998-05-06
56	PRIOR APPLICATION NUMBER: 60/084637
57	PRIOR FILING DATE: 1998-05-07
58	PRIOR APPLICATION NUMBER: 60/084639
59	PRIOR FILING DATE: 1998-05-07
60	PRIOR APPLICATION NUMBER: 60/084640
61	PRIOR FILING DATE: 1998-05-07
62	PRIOR APPLICATION NUMBER: 60/084627
63	PRIOR FILING DATE: 1998-05-07
64	PRIOR APPLICATION NUMBER: 60/084643
65	PRIOR FILING DATE: 1998-05-07
66	PRIOR APPLICATION NUMBER: 60/085339
67	PRIOR FILING DATE: 1998-05-13
68	PRIOR APPLICATION NUMBER: 60/085338
69	PRIOR FILING DATE: 1998-05-13


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, PRIOR APPLICATION NUMBER: 60/085689
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085579
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085580
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085573
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085704
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085697
, PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score
Best Local Similarity 48.6%; 19; M
Matches 53; Conservative

Qy 1 MEGAYGAGYAGGAGFDPYTLVRQPPH
Db 1 MESGAYGAARXAGGSFDRRLRFLTPQ
Qy 61 YNRPNACSGVAVGVLAFLATCLL
Db 61 FNRNEDACRYSAGVLAFLASAF

RESULT 7
US-09-999-832A-162
, Sequence 162, Application US/0999983
, Publication No. US20020192706A1
GENERAL INFORMATION:
, APPLICANT: Ashkenazi, Avi
, APPLICANT: Baker Kevin P.
, APPLICANT: Botstein, David
, APPLICANT: Denoyers, Luc
, APPLICANT: Eaton, Dan
, APPLICANT: Ferrara, Napoleon
, APPLICANT: Filvaroff, Ellen
, APPLICANT: Fong, Sherman
, APPLICANT: Gao, Wei-Qiang
, APPLICANT: Gerber, Hanspeter
, APPLICANT: Gerritsen, Mary E.
, APPLICANT: Goddard, Audrey
, APPLICANT: Godowski, Paul J.
, APPLICANT: Gromaldi, J. Christopher
, APPLICANT: Gurney, Austin L.
, APPLICANT: Hillan, Kenneth J.
, APPLICANT: Khlavin, Ivar J.
, APPLICANT: Kuo, Sophia S.
, APPLICANT: Napier, Mary A.
, APPLICANT: Pan, James;
, APPLICANT: Paoni, Nicholas F.
, APPLICANT: Roy, Margaret Ann
, APPLICANT: Shelton, David L.
, APPLICANT: Stewart, Timothy A.
, APPLICANT: Tumas, Daniel
, APPLICANT: Williams, P. Mickey
, APPLICANT: Wood, William I.
TITLE OF INVENTION: Secrated and Tr
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/9
CURRENT FILING DATE: 2001-10-24
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062255
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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 , PRIOR FILING DATE: 1998-05-15
 , PRIOR APPLICATION NUMBER: 60/085704
 , PRIOR FILING DATE: 1998-05-15
 , PRIOR APPLICATION NUMBER: 60/085697

Query Match	42.1%	Score 296;	DB 9;	Length 224;
Best Local Similarity	48.6%	Pred. No. 1.2e-25;		
Matches 53: Conservative	19;	Mismatches 37;	Indels	

Qy	1	MEGGAGACKAGAGADPYTLVROPHITLAVSWLFSIVVFGSIVNEGYLSNASEGEQFCI	60
Db <td>1 <td>MEGGAGAAKAGSGDLRRFLTPQVQKAVCLVFLALVFCITGEGYSNAHESKQMYCV <td>60</td> </td></td>	1 <td>MEGGAGAAKAGSGDLRRFLTPQVQKAVCLVFLALVFCITGEGYSNAHESKQMYCV <td>60</td> </td>	MEGGAGAAKAGSGDLRRFLTPQVQKAVCLVFLALVFCITGEGYSNAHESKQMYCV <td>60</td>	60
Qy <td>61 <td>YNRNPACSYGVAVGYLAFELTCLLYLALDVPYFQISSVKDRKKAYLSDI</td> <td>109</td> </td>	61 <td>YNRNPACSYGVAVGYLAFELTCLLYLALDVPYFQISSVKDRKKAYLSDI</td> <td>109</td>	YNRNPACSYGVAVGYLAFELTCLLYLALDVPYFQISSVKDRKKAYLSDI	109
Db <td>61 <td>FNRNEDACRYGSAIGVLAFLASAFVLVDVDFYFQISSNATDRKLYLVIGDL</td> <td>109</td> </td>	61 <td>FNRNEDACRYGSAIGVLAFLASAFVLVDVDFYFQISSNATDRKLYLVIGDL</td> <td>109</td>	FNRNEDACRYGSAIGVLAFLASAFVLVDVDFYFQISSNATDRKLYLVIGDL	109

RESULT 8

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US-09-378-189-162
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Trans
; TITLE OF INVENTION: Acids Encoding
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APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
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 APPLICANT: Kiljavin, Ivar J.
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 APPLICANT: Napier, Mary A.
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC4
 CURRENT APPLICATION NUMBER: US/09/978,191A
 CURRENT FILING DATE: 2001-10-15
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C25
CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918595
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7	PRIOR APPLICATION NUMBER: 60/085697

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RESULT 14
US-09-999-833A-162
; Sequence 162, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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APPLICANT: Hillan, Kenneth J
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P26301C65
 CURRENT APPLICATION NUMBER: US/09/999,833A
 CURRENT FILING DATE: 2001-10-24
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
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 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31

APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC12
 CURRENT APPLICATION NUMBER: US/09/981,915A
 CURRENT FILING DATE: 2001-10-16
 PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;

Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGAYGAGKAGGADPYTLVRPHILRWLFSIVVFGSTVNRGVLNSASEGRQFCI 60
DB 1 MEGAYGAKAGGSFDRFLTPQPVVARAVCLVFLVFCIYGGYNAHESKOMYCV 60
QY 61 YNRNPNACSYGVAVGVLAFELTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKVLVIGDL 109

RESULT 16

US-09-978-824-162
; Sequence 162, Application US/09978824
; Publication No. US2003005216A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/077450
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4	PRIOR FILING DATE: 1998-04-08
5	PRIOR APPLICATION NUMBER: 60/081049
6	PRIOR FILING DATE: 1998-04-08
7	PRIOR APPLICATION NUMBER: 60/081071
8	PRIOR FILING DATE: 1998-04-08
9	PRIOR APPLICATION NUMBER: 60/081195
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, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085704
, PRIOR FILING DATE: 1998-05-15
, PRIOR APPLICATION NUMBER: 60/085697

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Query Match 42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0;

Qy	1	MEGGAGACKAGCAGDPPYTLVROPHITLARVSWLFSIVVFGSIVNEGVYLSASEGEFCI	60
Db	1	MESGAGAAKAGGSDLRRLFTQPPQVARAVCLVFALLVFSCTVGEYSNAHESKQMYCV	60
Qy	61	YNRNPACSYGVAVGYLAFLTCLLYLALDLYVFPQISSVKRKKAVLSDI	109
Db	61	FNENEACRYGSAIGVLAFLASAFVLVDVAFVFPQISNATDRKYLVIIGDL	109

RESULT 17
US-09-918-585A-162
; Sequence 162, Application US/09918585A
; Publication No. US20030060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hansper
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C1
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; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
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; PRIOR APPLICATION NUMBER: 60/080165
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; PRIOR APPLICATION NUMBER: 60/081955
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; PRIOR APPLICATION NUMBER: 60/081952
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; PRIOR APPLICATION NUMBER: 60/082797
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; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07

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/	/	PRIOR APPLICATION NUMBER: 60/085339	
/	/	PRIOR FILING DATE: 1998-05-13	
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/	/	PRIOR APPLICATION NUMBER: 60/085323	
/	/	PRIOR FILING DATE: 1998-05-13	
/	/	PRIOR APPLICATION NUMBER: 60/085582	
/	/	PRIOR FILING DATE: 1998-05-15	
/	/	PRIOR APPLICATION NUMBER: 60/085700	
/	/	PRIOR FILING DATE: 1998-05-15	
/	/	PRIOR APPLICATION NUMBER: 60/085689	
/	/	PRIOR FILING DATE: 1998-05-15	
/	/	PRIOR APPLICATION NUMBER: 60/085579	
/	/	PRIOR FILING DATE: 1998-05-15	
/	/	PRIOR APPLICATION NUMBER: 60/085580	
/	/	PRIOR FILING DATE: 1998-05-15	
/	/	PRIOR APPLICATION NUMBER: 60/085573	
/	/	PRIOR FILING DATE: 1998-05-15	
/	/	PRIOR APPLICATION NUMBER: 60/085704	
/	/	PRIOR FILING DATE: 1998-05-15	
/	/	PRIOR APPLICATION NUMBER: 60/085697	
Query Match 42.1%; Score			
Best Local Similarity 48.6%; Pred			
Matches 53; Conservative 19; M			
Qy	1	MEGGAYGAGKAGGAFDPYTLVRQPP	: : : :
Db	1	MESGAYGAAXKAGGSFDLRRFLTPQ	: : : :
Qy	61	YNRPNKASGVAVGVLAFLITCLL	: : : :
Db	61	FRNEDACRYGSAIGVLAFLASAF	: : : :
RESULT 19			
US-09-978-423A-162			
; Sequence 162, Application US/0997842			
; Publication No. US20030069178A1			
GENERAL INFORMATION:			
APPLICANT: Ashkenazi, Avi			
APPLICANT: Baker Kevin P.			
APPLICANT: Borstein, David			
APPLICANT: Desnoyers, Luc			
APPLICANT: Eaton, Dan			
APPLICANT: Ferrara, Napoleon			
APPLICANT: Filvaroff, Ellen			
APPLICANT: Fong, Sherman			
APPLICANT: Gao, Wei-Qiang			
APPLICANT: Gerber, Hanspeter			
APPLICANT: Gerritsen, Mary E.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Grimaldi, J. Christophe			
APPLICANT: Gurney, Austin L.			
APPLICANT: Hillan, Kenneth J.			
APPLICANT: Klvajin, Ivar J.			
APPLICANT: Kuo, Sophia S.			
APPLICANT: Napier, Mary A.			
APPLICANT: Pan, James;			
APPLICANT: Paoni, Nicholas F.			
APPLICANT: Roy, Margaret Ann			
APPLICANT: Shelton, David L.			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Williams, P. Mickey			
APPLICANT: Wood, William I.			
TITLE OF INVENTION: Secreted and Tr			
TITLE OF INVENTION: Acids Encoding			
FILE REFERENCE: P2630P1C21			

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Query Match      42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy      1  MEGGAYGAGKAGAGDPYTLVROPHTILRVVSWLFSIVVFGSVTVNEGYNLSASEGEQFCI 60
      ||| ||| ||| ||| ||| : ||| : ||| : ||| ||| ||| ||| : ||| : ||| :
Db      1  MESGAYGAAGAGGSDFLRFLTPQVVARAVCLVFLVIFVSCIVGEGYNAHESKQMYCV 60
      : ||| : ||| ||| ||| : ||| : ||| ||| ||| ||| : ||| : ||| : ||| :
Qy      61  ENRNPNACSYGVAVGVLAFUTLCILYLALDLYVFPQISVVKRKKAVLSDI 109
      : ||| : ||| ||| ||| : ||| : ||| ||| ||| ||| : ||| : ||| : ||| :
Db      61  ENRNEDACRYGSAIGVLAFPLASAFFLWVDAYFPQISNATDRKYLVIIGDL 109
      : ||| : ||| ||| ||| : ||| : ||| ||| ||| ||| : ||| : ||| : ||| :

RESULT 19
US-09-378-423A-162
; Sequence 162, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C21

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; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFPPYTLVROPHILRVVSWLFSIVVFGSIVNVEGYLNSASEGEQFCI 60
DB 1 MESSGAYGAAGAGGSGFDRRLFTQPVVARAVCLVFLVFCIYSGYSNAHESKOMYCV 60

QY 61 YNRNPWACSGVAGVGLVFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDL 109

RESULT 20
US-09-978-193A-162
; Sequence 162, Application US/09978193A
; Publication No. US20030073624A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottfredsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC6
; CURRENT APPLICATION NUMBER: US/09/978,193A
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
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US-09-999-830A-162
; Sequence 162, Application US/09999830A
; Publication No. US20030077000A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumaq, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmitted
; FILE REFERENCE: P2630P1C70
; CURRENT APPLICATION NUMBER: US/09/999
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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[illegible]

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; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697  
  
Query Match          42.1%; Score 296; DB 10; Length 224;  
Best Local Similarity 48.6%; Pred. No. 1.2e-25;  
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;  
  
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Db      1 MESGAYGAAKAGGSFDRRLFTQPVVARAVCLVFALIVFSCTYGGYSNAHESKMVCV 60  
  
Qy      61 YRNPNCASYGVAVGLAFELTCLLYIALDVYPFPQISSVKDKRKAVLSDI 109  
        : : : : : ||| ||||| : : : ||||| : : : : :  
Db      61 FRNEDACRYGSAIGVLAFSLAFAFLVDVDAFFPQISNATDRKYLVIIDL 109  
  
RESULT 22  
US-09-378-757A-162  
; Sequence 162, Application US/09978757A  
; Publication No. US20030083248A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secrets and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C26  
; CURRENT APPLICATION NUMBER: US/09/978,757A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC2
CURRENT APPLICATION NUMBER: US/09/978,298A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Query Match 42.1%; Score 296; DB 10; Length 224;
 Best Local Similarity 48.6%; Pred. No. 1.2e-25;
 Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MEGGACAGCAGGAFDYTLVROPHILTRVSWLFSIVVGVGSIIVNGVLSASGEGQFCI 60
 Db 1 MEGGACAGCAGGAFDYTLVROPHILTRVSWLFSIVVGVGSIIVNGVLSASGEGQFCI 60
 Qy 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDKKAVLSDI 109
 Db 61 FNRNEDACRYGSAIGVLAFLASAFFLWVDVDFYQISNATDRKLVIGDL 109

RESULT 27
 US-09-978-188A-162
 ; Sequence 162, Application US/09978188A
 ; Publication No. US20030139328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C8
 ; CURRENT APPLICATION NUMBER: US/09/978,188A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGADPYTLVRPHTILRVSWLFSIVVFGSIWNEGYLNSASEGEQFCI 60
DB 1 MESSGAYGAAGKAGGSFDRFLPTQPVVARAVCLVFLIIVFSCIYGEQYSHAKSKQMYCV 60
QY 61 YNRPNACSYGVAAGVLAFILTCILLYLALDVIYFPQISSVKORKKXVLSDI 109
DB 61 FNEEDACRYGSAIGVLAFILASAFFLWVDVDAFFQISNATDRKYLVIQDL 109

RESULT 28
US-09-978-681A-162
; Sequence 162, Application US/09978681A
; Publication No. US20030195148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
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APPLICANT: Kljavin, Ivar J.
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APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC18
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
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PRIOR APPLICATION NUMBER: 60/082804
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PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29

7	PRIOR APPLICATION NUMBER: 60/083742	
7	PRIOR FILING DATE: 1998-04-30	
7	PRIOR APPLICATION NUMBER: 60/084366	
7	PRIOR FILING DATE: 1998-05-05	
7	PRIOR APPLICATION NUMBER: 60/084414	
7	PRIOR FILING DATE: 1998-05-06	
7	PRIOR APPLICATION NUMBER: 60/084441	
7	PRIOR FILING DATE: 1998-05-06	
7	PRIOR APPLICATION NUMBER: 60/084637	
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7	PRIOR APPLICATION NUMBER: 60/084639	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/084640	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/084627	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/084643	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/085339	
7	PRIOR FILING DATE: 1998-05-13	
7	PRIOR APPLICATION NUMBER: 60/085338	
7	PRIOR FILING DATE: 1998-05-13	
7	PRIOR APPLICATION NUMBER: 60/085323	
7	PRIOR FILING DATE: 1998-05-13	
7	PRIOR APPLICATION NUMBER: 60/085582	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085700	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085689	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085579	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085580	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085573	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085704	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085697	

RESULT 29
US-09-978-194A-162
; Sequence 162, Application US/09978194A
; Publication No. US20030195333A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

APPLICANT:	Godard, Audrey	
APPLICANT:	Godowski, Paul J.	
APPLICANT:	Grimaldi, J. Christopher	
APPLICANT:	Gurney, Austin L.	
APPLICANT:	Hillan, Kenneth J.	
APPLICANT:	Kljasin, Ivar J.	
APPLICANT:	Kuo, Sophia S.	
APPLICANT:	Napier, Mary A.	
APPLICANT:	Pan, James;	
APPLICANT:	Paoni, Nicholas P.	
APPLICANT:	Roy, Margaret Ann	
APPLICANT:	Shelton, David L.	
APPLICANT:	Stewart, Timothy A.	
APPLICANT:	Tumas, Daniel	
APPLICANT:	Williams, P. Mickey	
APPLICANT:	Wood, William I.	
TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic	
TITLE OF INVENTION:	Acids Encoding the Same	
FILE REFERENCE:	P2630PLC10	
CURRENT APPLICATION NUMBER:	US/09/978,194A	
CURRENT FILING DATE:	2001-10-15	
PRIOR APPLICATION NUMBER:	09/918585	
PRIOR FILING DATE:	2001-07-30	
PRIOR APPLICATION NUMBER:	60/062250	
PRIOR FILING DATE:	1997-10-17	
PRIOR APPLICATION NUMBER:	60/064249	
PRIOR FILING DATE:	1997-11-03	
PRIOR APPLICATION NUMBER:	60/065311	
PRIOR FILING DATE:	1997-11-13	
PRIOR APPLICATION NUMBER:	60/066364	
PRIOR FILING DATE:	1997-11-21	
PRIOR APPLICATION NUMBER:	60/077450	
PRIOR FILING DATE:	1998-03-10	
PRIOR APPLICATION NUMBER:	60/077632	
PRIOR FILING DATE:	1998-03-11	
PRIOR APPLICATION NUMBER:	60/077641	
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PRIOR APPLICATION NUMBER:	60/077649	
PRIOR FILING DATE:	1998-03-11	
PRIOR APPLICATION NUMBER:	60/077791	
PRIOR FILING DATE:	1998-03-12	
PRIOR APPLICATION NUMBER:	60/078004	
PRIOR FILING DATE:	1998-03-13	
PRIOR APPLICATION NUMBER:	60/078886	
PRIOR FILING DATE:	1998-03-20	
PRIOR APPLICATION NUMBER:	60/078936	
PRIOR FILING DATE:	1998-03-20	
PRIOR APPLICATION NUMBER:	60/078910	
PRIOR FILING DATE:	1998-03-20	
PRIOR APPLICATION NUMBER:	60/078939	
PRIOR FILING DATE:	1998-03-20	
PRIOR APPLICATION NUMBER:	60/079294	
PRIOR FILING DATE:	1998-03-25	
PRIOR APPLICATION NUMBER:	60/079656	
PRIOR FILING DATE:	1998-03-26	
PRIOR APPLICATION NUMBER:	60/079664	
PRIOR FILING DATE:	1998-03-27	
PRIOR APPLICATION NUMBER:	60/079689	
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PRIOR APPLICATION NUMBER:	60/079863	
PRIOR FILING DATE:	1998-03-27	
PRIOR APPLICATION NUMBER:	60/079728	
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PRIOR FILING DATE:	1998-03-27	
PRIOR APPLICATION NUMBER:	60/079920	
PRIOR FILING DATE:	1998-03-30	
PRIOR APPLICATION NUMBER:	60/079923	
PRIOR FILING DATE:	1998-03-30	
PRIOR APPLICATION NUMBER:	60/080105	
PRIOR FILING DATE:	1998-03-31	
PRIOR APPLICATION NUMBER:	60/080107	
PRIOR FILING DATE:	1998-03-31	

PRIOR APPLICATION NUMBER:	09/918589
PRIOR FILING DATE:	2001-07-30
PRIOR APPLICATION NUMBER:	60/062250
PRIOR FILING DATE:	1997-10-17
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PRIOR FILING DATE:	1998-03-25
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PRIOR FILING DATE:	1998-03-31
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PRIOR FILING DATE:	1998-03-31
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PRIOR APPLICATION NUMBER:	60/080334
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/080328
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PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081195
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081203

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; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR APPLICATION NUMBER: 60/085580
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGADPDYTLVROPHTILRWMLFSIVVFGSTVNEGYNLSASEGGEQFCI 60
Db 1 MESGAYGAAGAGGSFDRFLTPQVVARAVCLVFLIVFSCIYGGYSNAHESKOMYCV 60

QY 61 YNRPNACSGVAGVGLAFITCLLYLALDVFYFQISSVKDRKKAVLSDI 109
Db 61 FPNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKVLVIGDL 109

RESULT 33
US-09-978-665A-162
; Sequence 162, Application US/09978665A
; Publication No. US20030159437A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C19
; CURRENT APPLICATION NUMBER: US/09/978, 665A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-08
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
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1	PRIOR FILING DATE: 1998-04-15	
2	PRIOR APPLICATION NUMBER: 60/081819	
3	PRIOR FILING DATE: 1998-04-15	
4	PRIOR APPLICATION NUMBER: 60/081952	
5	PRIOR FILING DATE: 1998-04-15	
6	PRIOR APPLICATION NUMBER: 60/081838	
7	PRIOR FILING DATE: 1998-04-15	
8	PRIOR APPLICATION NUMBER: 60/082568	
9	PRIOR FILING DATE: 1998-04-21	
10	PRIOR APPLICATION NUMBER: 60/082569	
11	PRIOR FILING DATE: 1998-04-21	
12	PRIOR APPLICATION NUMBER: 60/082704	
13	PRIOR FILING DATE: 1998-04-22	
14	PRIOR APPLICATION NUMBER: 60/082804	
15	PRIOR FILING DATE: 1998-04-22	
16	PRIOR APPLICATION NUMBER: 60/082700	
17	PRIOR FILING DATE: 1998-04-22	
18	PRIOR APPLICATION NUMBER: 60/082797	
19	PRIOR FILING DATE: 1998-04-22	
20	PRIOR APPLICATION NUMBER: 60/082796	
21	PRIOR FILING DATE: 1998-04-23	
22	PRIOR APPLICATION NUMBER: 60/083336	
23	PRIOR FILING DATE: 1998-04-27	
24	PRIOR APPLICATION NUMBER: 60/083322	
25	PRIOR FILING DATE: 1998-04-28	
26	PRIOR APPLICATION NUMBER: 60/083392	
27	PRIOR FILING DATE: 1998-04-29	
28	PRIOR APPLICATION NUMBER: 60/083495	
29	PRIOR FILING DATE: 1998-04-29	
30	PRIOR APPLICATION NUMBER: 60/083496	
31	PRIOR FILING DATE: 1998-04-29	
32	PRIOR APPLICATION NUMBER: 60/083499	
33	PRIOR FILING DATE: 1998-04-29	
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37	PRIOR FILING DATE: 1998-04-29	
38	PRIOR APPLICATION NUMBER: 60/083558	
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41	PRIOR FILING DATE: 1998-04-29	
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43	PRIOR FILING DATE: 1998-04-29	
44	PRIOR APPLICATION NUMBER: 60/083742	
45	PRIOR FILING DATE: 1998-04-30	
46	PRIOR APPLICATION NUMBER: 60/084366	
47	PRIOR FILING DATE: 1998-05-05	
48	PRIOR APPLICATION NUMBER: 60/084414	
49	PRIOR FILING DATE: 1998-05-06	
50	PRIOR APPLICATION NUMBER: 60/084441	
51	PRIOR FILING DATE: 1998-05-06	
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53	PRIOR FILING DATE: 1998-05-07	
54	PRIOR APPLICATION NUMBER: 60/084639	
55	PRIOR FILING DATE: 1998-05-07	
56	PRIOR APPLICATION NUMBER: 60/084640	
57	PRIOR FILING DATE: 1998-05-07	
58	PRIOR APPLICATION NUMBER: 60/084598	
59	PRIOR FILING DATE: 1998-05-07	
60	PRIOR APPLICATION NUMBER: 60/084600	
61	PRIOR FILING DATE: 1998-05-07	
62	PRIOR APPLICATION NUMBER: 60/084627	
63	PRIOR FILING DATE: 1998-05-07	
64	PRIOR APPLICATION NUMBER: 60/084643	
65	PRIOR FILING DATE: 1998-05-07	
66	PRIOR APPLICATION NUMBER: 60/085339	
67	PRIOR FILING DATE: 1998-05-13	
68	PRIOR APPLICATION NUMBER: 60/085338	
69	PRIOR FILING DATE: 1998-05-13	
70	PRIOR APPLICATION NUMBER: 60/085323	
71	PRIOR FILING DATE: 1998-05-13	
72	PRIOR APPLICATION NUMBER: 60/085582	
73	PRIOR FILING DATE: 1998-05-15	

1 PRIOR APPLICATION NUMBER: 60/085700
2 PRIOR FILING DATE: 1998-05-15
3 PRIOR APPLICATION NUMBER: 60/085689
4 PRIOR FILING DATE: 1998-05-15
5 PRIOR APPLICATION NUMBER: 60/085579
6 PRIOR FILING DATE: 1998-05-15
7 PRIOR APPLICATION NUMBER: 60/085580
8 PRIOR FILING DATE: 1998-05-15
9 PRIOR APPLICATION NUMBER: 60/085573
10 PRIOR FILING DATE: 1998-05-15
11 PRIOR APPLICATION NUMBER: 60/085704
12 PRIOR FILING DATE: 1998-05-15
13 PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 10; Length 224;
Best Local Similarity 48.8%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPTLVROPHITLVRVSWLFSIVVFGSIVNBSYGEQFCI 60
Db 1 MEGGAYGAGKAGGAFDPTLVROPHITLVRVSWLFSIVVFGSIVNBSYGEQFCI 60
QY 61 YNRNPACSYGVAVGLAFITLCLLYALDVPFQISSVDRKKAIVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDVDFQISSVDRKKAIVLSDI 109

RESULT 35
US-09-999-831A-162
Sequence 162, Application US/09999831A
Publication No. US20040048332A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Sheiton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C68
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 162
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-09-999-831A-162
Query Match 42.1%; Score 296; DB 11; Length 224;

Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPTLVROPHITLVRVSWLFSIVVFGSIVNBSYGEQFCI 60
Db 1 MEGGAYGAGKAGGAFDPTLVROPHITLVRVSWLFSIVVFGSIVNBSYGEQFCI 60
QY 61 YNRNPACSYGVAVGLAFITLCLLYALDVPFQISSVDRKKAIVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDVDFQISSVDRKKAIVLSDI 109

RESULT 36
US-09-978-824-162
Sequence 162, Application US/09978824
Publication No. US20050124789A9
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Sheiton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C14
CURRENT FILING DATE: 2001-10-17
CURRENT APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20

1 PRIOR APPLICATION NUMBER: 60/078936
2 PRIOR FILING DATE: 1998-03-20
3 PRIOR APPLICATION NUMBER: 60/078910
4 PRIOR FILING DATE: 1998-03-20
5 PRIOR APPLICATION NUMBER: 60/078939
6 PRIOR FILING DATE: 1998-03-20
7 PRIOR APPLICATION NUMBER: 60/079294
8 PRIOR FILING DATE: 1998-03-25
9 PRIOR APPLICATION NUMBER: 60/079656
10 PRIOR FILING DATE: 1998-03-26
11 PRIOR APPLICATION NUMBER: 60/079664
12 PRIOR FILING DATE: 1998-03-27
13 PRIOR APPLICATION NUMBER: 60/079689
14 PRIOR FILING DATE: 1998-03-27
15 PRIOR APPLICATION NUMBER: 60/079663
16 PRIOR FILING DATE: 1998-03-27
17 PRIOR APPLICATION NUMBER: 60/079728
18 PRIOR FILING DATE: 1998-03-27
19 PRIOR APPLICATION NUMBER: 60/079786
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21 PRIOR APPLICATION NUMBER: 60/079920
22 PRIOR FILING DATE: 1998-03-30
23 PRIOR APPLICATION NUMBER: 60/079923
24 PRIOR FILING DATE: 1998-03-30
25 PRIOR APPLICATION NUMBER: 60/080105
26 PRIOR FILING DATE: 1998-03-31
27 PRIOR APPLICATION NUMBER: 60/080107
28 PRIOR FILING DATE: 1998-03-31
29 PRIOR APPLICATION NUMBER: 60/080165
30 PRIOR FILING DATE: 1998-03-31
31 PRIOR APPLICATION NUMBER: 60/080194
32 PRIOR FILING DATE: 1998-03-31
33 PRIOR APPLICATION NUMBER: 60/080327
34 PRIOR FILING DATE: 1998-04-01
35 PRIOR APPLICATION NUMBER: 60/080328
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38 PRIOR FILING DATE: 1998-04-01
39 PRIOR APPLICATION NUMBER: 60/080334
40 PRIOR FILING DATE: 1998-04-01
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42 PRIOR FILING DATE: 1998-04-08
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45 PRIOR APPLICATION NUMBER: 60/081071
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50 PRIOR FILING DATE: 1998-04-09
51 PRIOR APPLICATION NUMBER: 60/081229
52 PRIOR FILING DATE: 1998-04-09
53 PRIOR APPLICATION NUMBER: 60/081955
54 PRIOR FILING DATE: 1998-04-15
55 PRIOR APPLICATION NUMBER: 60/081817
56 PRIOR FILING DATE: 1998-04-15
57 PRIOR APPLICATION NUMBER: 60/081819
58 PRIOR FILING DATE: 1998-04-15
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60 PRIOR FILING DATE: 1998-04-15
61 PRIOR APPLICATION NUMBER: 60/081838
62 PRIOR FILING DATE: 1998-04-15
63 PRIOR APPLICATION NUMBER: 60/082568
64 PRIOR FILING DATE: 1998-04-21
65 PRIOR APPLICATION NUMBER: 60/082569
66 PRIOR FILING DATE: 1998-04-21
67 PRIOR APPLICATION NUMBER: 60/082704
68 PRIOR FILING DATE: 1998-04-22
69 PRIOR APPLICATION NUMBER: 60/082804
70 PRIOR FILING DATE: 1998-04-22
71 PRIOR APPLICATION NUMBER: 60/082700
72 PRIOR FILING DATE: 1998-04-22
73 PRIOR APPLICATION NUMBER: 60/082797

74 PRIOR FILING DATE: 1998-04-22
75 PRIOR APPLICATION NUMBER: 60/082796
76 PRIOR FILING DATE: 1998-04-23
77 PRIOR APPLICATION NUMBER: 60/083336
78 PRIOR FILING DATE: 1998-04-27
79 PRIOR APPLICATION NUMBER: 60/083322
80 PRIOR FILING DATE: 1998-04-28
81 PRIOR APPLICATION NUMBER: 60/083392
82 PRIOR FILING DATE: 1998-04-29
83 PRIOR APPLICATION NUMBER: 60/083495
84 PRIOR FILING DATE: 1998-04-29
85 PRIOR APPLICATION NUMBER: 60/083496
86 PRIOR FILING DATE: 1998-04-29
87 PRIOR APPLICATION NUMBER: 60/083499
88 PRIOR FILING DATE: 1998-04-29
89 PRIOR APPLICATION NUMBER: 60/083545
90 PRIOR FILING DATE: 1998-04-29
91 PRIOR APPLICATION NUMBER: 60/083554
92 PRIOR FILING DATE: 1998-04-29
93 PRIOR APPLICATION NUMBER: 60/083558
94 PRIOR FILING DATE: 1998-04-29
95 PRIOR APPLICATION NUMBER: 60/083559
96 PRIOR FILING DATE: 1998-04-29
97 PRIOR APPLICATION NUMBER: 60/083500
98 PRIOR FILING DATE: 1998-04-29
99 PRIOR APPLICATION NUMBER: 60/083742
100 PRIOR FILING DATE: 1998-04-30
101 PRIOR APPLICATION NUMBER: 60/084366
102 PRIOR FILING DATE: 1998-05-05
103 PRIOR APPLICATION NUMBER: 60/084414
104 PRIOR FILING DATE: 1998-05-06
105 PRIOR APPLICATION NUMBER: 60/084441
106 PRIOR FILING DATE: 1998-05-06
107 PRIOR APPLICATION NUMBER: 60/084637
108 PRIOR FILING DATE: 1998-05-07
109 PRIOR APPLICATION NUMBER: 60/084639
110 PRIOR FILING DATE: 1998-05-07
111 PRIOR APPLICATION NUMBER: 60/084640
112 PRIOR FILING DATE: 1998-05-07
113 PRIOR APPLICATION NUMBER: 60/084598
114 PRIOR FILING DATE: 1998-05-07
115 PRIOR APPLICATION NUMBER: 60/084600
116 PRIOR FILING DATE: 1998-5-07
117 PRIOR APPLICATION NUMBER: 60/084627
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120 PRIOR FILING DATE: 1998-05-07
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123 PRIOR APPLICATION NUMBER: 60/085338
124 PRIOR FILING DATE: 1998-05-13
125 PRIOR APPLICATION NUMBER: 60/085323
126 PRIOR FILING DATE: 1998-05-13
127 PRIOR APPLICATION NUMBER: 60/085582
128 PRIOR FILING DATE: 1998-05-15
129 PRIOR APPLICATION NUMBER: 60/085700
130 PRIOR FILING DATE: 1998-05-15
131 PRIOR APPLICATION NUMBER: 60/085689
132 PRIOR FILING DATE: 1998-05-15
133 PRIOR APPLICATION NUMBER: 60/085579
134 PRIOR FILING DATE: 1998-05-15
135 PRIOR APPLICATION NUMBER: 60/085580
136 PRIOR FILING DATE: 1998-05-15
137 PRIOR APPLICATION NUMBER: 60/085573
138 PRIOR FILING DATE: 1998-05-15
139 PRIOR APPLICATION NUMBER: 60/085704
140 PRIOR FILING DATE: 1998-05-15
141 PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 12; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLSASGEQFCI 60
DB 1 MESGAYGAAGAGGSGFLLRRFLTQPVVARAVCLVFLVFSICVYGGYSNAHESKQYCV 60
QY 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVDVYFPQISNATDRKYLVIIGDL 109

RESULT 37
US-10-017-081A-162
; Sequence 162, Application US/10017081A
; Publication No. US20030049684A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE REFERENCE: P2630P1C69
; CURRENT APPLICATION NUMBER: US/10/017,081A
; CURRENT FILING DATE: 2002-04-30
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-081A-162

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLSASGEQFCI 60
DB 1 MESGAYGAAGAGGSGFLLRRFLTQPVVARAVCLVFLVFSICVYGGYSNAHESKQYCV 60
QY 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVDVYFPQISNATDRKYLVIIGDL 109

RESULT 38
US-10-167-749-162
; Sequence 162, Application US/10167749
; Publication No. US20030056137A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE REFERENCE: P2630P1C60
; CURRENT APPLICATION NUMBER: US/10/167,749
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-167-749-162

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHTILRVVSWLFSIVVFGSIVNEGYLSASGEQFCI 60
DB 1 MESGAYGAAGAGGSGFLLRRFLTQPVVARAVCLVFLVFSICVYGGYSNAHESKQYCV 60
QY 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVDVYFPQISNATDRKYLVIIGDL 109
RESULT 39

US-10-013-921A-162
; Sequence 162, Application US/10013921A
; Publication No. US20030068648A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: F2630PIC84
; CURRENT APPLICATION NUMBER: US/10/013,921A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
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; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
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; PRIOR APPLICATION NUMBER: 60/084627
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; PRIOR APPLICATION NUMBER: 60/084643
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; PRIOR APPLICATION NUMBER: 60/085339
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; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MEGAYGAGKAGGAFDPTVLVROPHTILRVVSWLFSIVWFGSIWEGYLSASGEQFCI 60
Db 1 MEGAYGAGKAGGDFDRLRFITQVVARVCLVFLVISCYGEYSNAHESKQYCV 60
Qy 61 YRRNPACSYGAVGVGLAFILTLCLLYLALDVYFPQISSVKDKKAVLSDI 109
Db 61 FRRNEDACRYSGAIGVLAFSLASFVLDVDFPQISNATDRKYLVIIGDL 109

RESULT 40
US-10-013-929A-162
; Sequence 162, Application US/10013929A
; Publication No. US20030072745A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC89
; CURRENT APPLICATION NUMBER: US/10/013,929A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27

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1	PRIOR FILING DATE: 1998-04-29	60/083554
2	PRIOR APPLICATION NUMBER: 60/083554	
3	PRIOR FILING DATE: 1998-04-29	60/083558
4	PRIOR APPLICATION NUMBER: 60/083558	
5	PRIOR FILING DATE: 1998-04-29	60/083559
6	PRIOR APPLICATION NUMBER: 60/083559	
7	PRIOR FILING DATE: 1998-04-29	60/083500
8	PRIOR APPLICATION NUMBER: 60/083500	
9	PRIOR FILING DATE: 1998-04-29	60/083742
10	PRIOR APPLICATION NUMBER: 60/083742	
11	PRIOR FILING DATE: 1998-04-30	60/084366
12	PRIOR APPLICATION NUMBER: 60/084366	
13	PRIOR FILING DATE: 1998-05-05	60/084414
14	PRIOR APPLICATION NUMBER: 60/084414	
15	PRIOR FILING DATE: 1998-05-06	60/084441
16	PRIOR APPLICATION NUMBER: 60/084441	
17	PRIOR FILING DATE: 1998-05-06	60/084637
18	PRIOR APPLICATION NUMBER: 60/084637	
19	PRIOR FILING DATE: 1998-05-07	60/084639
20	PRIOR APPLICATION NUMBER: 60/084639	
21	PRIOR FILING DATE: 1998-05-07	60/084640
22	PRIOR APPLICATION NUMBER: 60/084640	
23	PRIOR FILING DATE: 1998-05-07	60/084598
24	PRIOR APPLICATION NUMBER: 60/084598	
25	PRIOR FILING DATE: 1998-05-07	60/084600
26	PRIOR APPLICATION NUMBER: 60/084600	
27	PRIOR FILING DATE: 1998-05-07	60/084627
28	PRIOR APPLICATION NUMBER: 60/084627	
29	PRIOR FILING DATE: 1998-05-07	60/084643
30	PRIOR APPLICATION NUMBER: 60/084643	
31	PRIOR FILING DATE: 1998-05-07	60/085339
32	PRIOR APPLICATION NUMBER: 60/085339	
33	PRIOR FILING DATE: 1998-05-13	60/085338
34	PRIOR APPLICATION NUMBER: 60/085338	
35	PRIOR FILING DATE: 1998-05-13	60/085323
36	PRIOR APPLICATION NUMBER: 60/085323	
37	PRIOR FILING DATE: 1998-05-13	60/085582
38	PRIOR APPLICATION NUMBER: 60/085582	
39	PRIOR FILING DATE: 1998-05-15	60/085700
40	PRIOR APPLICATION NUMBER: 60/085700	
41	PRIOR FILING DATE: 1998-05-15	60/085689
42	PRIOR APPLICATION NUMBER: 60/085689	
43	PRIOR FILING DATE: 1998-05-15	60/085573
44	PRIOR APPLICATION NUMBER: 60/085573	
45	PRIOR FILING DATE: 1998-05-15	60/085704
46	PRIOR APPLICATION NUMBER: 60/085704	
47	PRIOR FILING DATE: 1998-05-15	60/085697
48	PRIOR APPLICATION NUMBER: 60/085697	

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0;

Qy	1	MEGGAGACKAGGADPPYTLVQPHITLRVSWLSFISIVVFGSIVNEGYSINASGEQECI	60
Db	1	MEGGAGAAKAGGSDRLRFLTPQPVQAVRACLIVFALLVFCIYEGYSNAHESKQMYCV	60
Qy	61	YNRNPACSYGVAVGVLAFLTCLLYALDVPYFQISSVKDRKAVLSDI	109
Db	61	FNRENDACRYGSAIGVLAFLASAFVLVDVAYFQISNATDRKYLVIIGDL	109

RESULT 41
US-10-016-177A-162
; Sequence 162, Application US/10016177A
; Publication No. US20030073131A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.


```

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC59
; CURRENT FILING DATE: 2001-10-19
; CURRENT APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01

; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC59
; CURRENT FILING DATE: 2001-10-19
; CURRENT APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGAYGAGKAGGAFDPTLVROPHTLRVVSWMFISVVFSGIVNFGYLSASEGQFCI 60
Db 1 MEGAYGAAGAGSGFDRRLRFTQPVVARAVCLVFLVIFVSCIVGEGYSNAHESKQMCV 60

QY 61 YNRPNACSYGVAVGVLAFTLCILYLDVYFPQISSVKDKRKAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFSLASAFFLVVDAYFPQISNATDRKYLVIQDL 109

RESULT 42
US-10-166-709A-162
; Sequence 162, Application US/10166709A
; Publication No. US20030104536A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.

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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C39
; CURRENT APPLICATION NUMBER: US/10/143.031A
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/077791
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-031A-162

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNEGYNLSASGEQFCI 60
Db 1 MESSGAYGAAGAGGSFLLRRFLTPQVWARAVCLVFLVFCIYGEYSNAHESKQMYCV 60

QY 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVFPQISSVKDRKKAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFVLVDVDFPQISNATDRKYLVIIGDL 109

RESULT 44
US-10-143-030A-162
; Sequence 162, Application US/10143030A
; Publication No. US20030147901A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurnev, Austin L.

; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C33
; CURRENT APPLICATION NUMBER: US/10/143.030A
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-030A-162

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHILRVVSWLFSIVVFGSIVNEGYNLSASGEQFCI 60
Db 1 MESSGAYGAAGAGGSFLLRRFLTPQVWARAVCLVFLVFCIYGEYSNAHESKQMYCV 60

QY 61 YNRPNACSYGVAVGVLAFLTCLLYLALDVFPQISSVKDRKKAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFVLVDVDFPQISNATDRKYLVIIGDL 109

RESULT 45
US-10-002-967A-162
; Sequence 162, Application US/10002967A
; Publication No. US20030148373A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

```

; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PIC72
 ; CURRENT APPLICATION NUMBER: US/10/002,967A
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077641
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077649
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077791
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/078004
 ; PRIOR FILING DATE: 1998-03-13
 ; PRIOR APPLICATION NUMBER: 60/078886
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078936
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078939
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079656
 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079664
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 ; PRIOR APPLICATION NUMBER: 60/083500
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 ; PRIOR APPLICATION NUMBER: 60/083742
 ; PRIOR FILING DATE: 1998-04-30

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC67
CURRENT APPLICATION NUMBER: US/10/017, 083A
CURRENT FILING DATE: 2001-10-24
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 162
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-083A-162

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPTLVROPHTILRVVSWLFSIVVFGSIVNEGYNLSASEGQFCI 60
Db 1 MESSAYGAAGKAGGSDLRRLTQPQVVARAVCLVFLVFCIVGEGYSNAHESKQMYCV 60
QY 61 YNRNPACSYGVAVGVLAFTCLLYLALDVYFPQISSVKDKKAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109

RESULT 46
US-10-017-083A-162
Sequence 162, Application US/10017083A
Publication No. US20030148376A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC67
CURRENT APPLICATION NUMBER: US/10/017, 083A
CURRENT FILING DATE: 2001-10-24
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 624
SEQ ID NO 162
LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-083A-162

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPTLVROPHTILRVVSWLFSIVVFGSIVNEGYNLSASEGQFCI 60
Db 1 MESSAYGAAGKAGGSDLRRLTQPQVVARAVCLVFLVFCIVGEGYSNAHESKQMYCV 60
QY 61 YNRNPACSYGVAVGVLAFTCLLYLALDVYFPQISSVKDKKAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109

RESULT 47
US-10-145-128A-162
Sequence 162, Application US/10145128A
Publication No. US20030157615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC46
; CURRENT APPLICATION NUMBER: US/10/145,128A
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR APPLICATION NUMBER: 60/077632
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; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 162
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-128A-162

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Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

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QY 1 MEGGAGAGAGAGADPYTLVROPHITLWVSLFSLVVGSTVNEGYLNSASEGQFCI 60
Db 1 MESGAYGAKAGGSFDRFLTPQVVARAVCLVFLVFCIYGGYNAHESKOMYCV 60
QY 61 YNRPNACSYGAVGVGLAFITLCLLYLALDVPFQISSVKDRKKAIVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDKRYLVIGDL 109

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RESULT 48
US-10-017-191A-162
; Sequence 162, Application US/10017191A
; Publication No. US20030170254A1
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.

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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC62
; CURRENT APPLICATION NUMBER: US/10/017,191A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085580
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAGACKAGGADPYTLVRQPHILRWLFWLFGIVVFGSTVNRGYNLSASEGQFCI 60
DB 1 MSGAYGAAGAGGSDLRRLTQPQVVARAVCLVFLVFCIYGBYNAHESKQMYCV 60
QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDI 109
DB 61 FNRNEDACHYGSAGVLAFLASAFFLVVDAYFPQISNATDRKYLVIIGDL 109

RESULT 49
US-10-143-028A-162
; Sequence 162, Application US/10143028A
; Publication No. US20030180310A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

```

; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC37
; CURRENT APPLICATION NUMBER: US/10/143,028A
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC54
; CURRENT APPLICATION NUMBER: US/10/143,029A
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01

Query Match 42.1%; Score 296; DB 14; Length 224;
Best Local Similarity 48.6%; Pred. No. 1.2e-25;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGACAGKAGAPDYTLVRQPHILRWLFSIVVGSIVNREGYLNASGEQFCI 60
Db 1 MESSGAGAAKAGGSFDRFLTPQPVVARAVCLVFALIVFCIYSGYSNAHESKQMCV 60

QY 61 YNRNNACSGVAGVGLVAFLTCLLYLALDVYFPQISSVDRKKAVLSDI 109
Db 61 FNRNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKVLVIGDL 109

RESULT 50
US-10-143-029A-162
; Sequence 162, Application US/10143029A
; Publication No. US20030180311A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.

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T14897
probable ATPase (EC 3.6.1.-) - Leishmania donovani
C:Species: Leishmania donovani
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14897
R:Meade, J.C.; Xue, L.; Case, S.T.
A:Description: Leishmania donovani contains a family of p-type ion motive ATPase genes.
A:Reference number: Z18256
A:Accession: T14897
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1047 <MEA>
A:Cross-references: UNIPROT:O61136; EMBL:AF067495; NID:g3192902; PID:g3192903; PIDN:AACT1
A:Gene: CAl
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: hydrolase; ion transport
F:577-751/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 10.4%; Score 73.5; DB 2; Length 1047;
Best Local Similarity 30.3%; Pred. No. 29;
Matches 30; Conservative 16; Mismatches 38; Indels 15; Gaps 6;

QY 5 AYAGKAGGAFDPTLVROPHTILRVSWLFSIVFGSIWNEG-----YLSASEGEQ 57
DB 871 AFGLYFGLLIHSYT-VRPRVSIPIRMWLDNKNWIFGCVLGGALFVPVIYINAIHG-- 927

QY 58 FCIYRNPNACSGV-AVGVLAPLT-CLLYLAL-DVFFP 93
DB 928 --LFVHSMITWGVAVGVTPLAICETVKVIRNLFPP 964

RESULT 7
VCBBFH
N:Contains: coat protein precursor - flock house virus
N:Contains: coat protein alpha; coat protein beta; coat protein gamma
C:Species: flock house virus
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: B34011; S11037
R:Dasgupta, R.; Sgro, J.Y.
Nucleic Acids Res. 17, 7525-7526, 1989
A:Title: Nucleotide sequences of three nodavirus RNA2's: the messenger for their coat protein precursor and the coat protein gene
A:Reference number: A34011; MUID:90016821; PMID:2798110
A:Accession: B34011
A:Molecule type: genomic RNA
A:Residues: 1-407 <DAS>
A:Cross-references: UNIPROT:P12870; EMBL:X15959; NID:g59265; PIDN:CAA34081.1; PID:g59266
R:Kaesberg, P.; Dasgupta, R.; Sgro, J.Y.; Wery, J.P.; Selling, B.H.; Hosur, M.V.; Johnson, J. Mol. Biol. 214, 423-435, 1990
A:Title: Structural homology among four nodaviruses as deduced by sequencing and X-ray crystallography
A:Reference number: S11036; MUID:90339486; PMID:2116525
A:Contents: annotation
C:Genetics:
A:Map position: segment 2
C:Superfamily: black beetle virus coat protein
C:Keywords: coat protein; RNA binding
F:1-407/Product: coat protein alpha #status predicted <ALP>
F:1-363/Product: coat protein beta #status predicted <BET>
F:35-49/Region: arginine-rich RNA-binding pattern
F:364-407/Product: coat protein gamma #status predicted <GAM>
F:363-364/Cleavage site: Asn-Ala (autolytic) #status predicted

Query Match 10.4%; Score 73; DB 1; Length 407;
Best Local Similarity 28.9%; Pred. No. 12;
Matches 35; Conservative 15; Mismatches 57; Indels 14; Gaps 5;

QY 12 GGAFDPTLVROPHTILRVSW--LFSIVFGSIWNEGSGEQFCI-YRNPNAC 68
DB 270 GSTGQPTMDSGAATSGVGVGNMNTIVIRVS-APEGAVNSAILKAWSCIEVRPNAM 328
QY 69 SYGVA-----YGVLAFLTCLLYLALDVVFPQISSVKDRKAVL--SDIGVSGEPHPA 118

DB 329 LYQFGHDSPLDEVALQBYRTVARSPLVAVIAAQNASWVERVKSIIKSSLAASNIPGPI 388
QY 119 G 119
DB 389 G 389

RESULT 8
OOOCG
rhodopsin - giant octopus
C:Species: Octopus dofleini (giant octopus)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: S00610
R:Ovchinnikov, Y.A.; Abdulaev, N.G.; Zolotarev, A.S.; Artamonov, I.D.; Bessalov, I.A.; De FBBS Lett. 232, 69-72, 1988
A:Title: Octopus rhodopsin. Amino acid sequence deduced from cDNA.
A:Reference number: S00610; MUID:88211678; PMID:3366250
A:Accession: S00610
A:Molecule type: mRNA
A:Residues: 1-455 <OVC>
A:Cross-references: UNIPROT:P09241; EMBL:X07797
A:Note: the source is designated as Paroctopus defleini
A:Note: part of this sequence was confirmed by protein sequencing
C:Superfamily: octopus rhodopsin
C:Keywords: chromoprotein; color vision; G protein-coupled receptor; glycoprotein; lipoprotein
F:37-61/Domain: transmembrane #status predicted <TM1>
F:74-98/Domain: transmembrane #status predicted <TM2>
F:107-131/Domain: transmembrane #status predicted <TM3>
F:153-177/Domain: transmembrane #status predicted <TM4>
F:201-224/Domain: transmembrane #status predicted <TM5>
F:263-286/Domain: transmembrane #status predicted <TM6>
F:302-323/Domain: transmembrane #status predicted <TM7>
F:9,15/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:306/Binding site: retinal (Lys) (covalent) #status predicted
F:337,338/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 10.4%; Score 73; DB 1; Length 455;
Best Local Similarity 24.6%; Pred. No. 14;
Matches 31; Conservative 21; Mismatches 38; Indels 36; Gaps 6;

QY 9 GKAGGAF-----DPYTLVRQHTILRVVS-----MLFSIV-----V 39
DB 113 GLLGGIFGMSINTWAMISIDRYNIGRPMASKKMSHRRAFIMLIFVWMSLIVWSVGPV 172
QY 40 F--GSIVNEGYNLASEGEQFCIYRNPNACSYGVAVGLAFILTLCLLYLALDVVFPQISS 97
DB 173 FHWGAVVPEGLITSCS----FDYLTDPSTRFILLCMYFCGFWLPIIIIAF-CYFNIVMS 227
QY 98 VKDRKK 103
DB 228 VSNHEK 233

RESULT 9
S49489
trypsin (EC 3.4.21.4) precursor - Paranotothenia magellanica
C:Species: Paranotothenia magellanica
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S49489
R:Genicot, S.; Rentier-Delrue, F.; Edwards, D.; van Beeumen, J.; Dodson, G.; Gerday, C.
Submitted to the EMBL Data Library, October 1994
A:Description: Trypsin and trypsinogen from an antarctic fish: molecular basis of cold A:Reference number: S49489
A:Accession: S49489
A:Molecule type: mRNA
A:Residues: 1-242 <GEN>
A:Cross-references: UNIPROT:Q92099; EMBL:X82223; NID:g59507; PIDN:CAA57701.1; PID:g59595
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-13/Domain: signal sequence #status predicted <SIG>
F:14-242/Product: trypsin #status predicted <MAT>
F:21-235/Domain: trypsin homology <TRY>

Best Local Similarity 26.0%; Pred. No. 17;
Matches 39; Conservative 19; Mismatches 51; Indels 41; Gaps 9;

QY 14 AFDPTLVLPQPHILR-----VSWLFSIVV-FGSIYNEGVLNSASGEQF 58
DB 129 AVDRYLAVTNP-----LRYGLTVTKRRARAVALVIVSATVSPFAPIMSQWRVGDADAEQ 185

QY 59 CIYNNRPNACS-----YGVAVGVLAFLTCLLYLALDVFPQITSSVDRKKAVLSIDIG-- 110
DB 186 C--HSNPRCCSPASNMPYALLSSVSFYLPLAVM-LFVYARVFAKQRFRVRELGRF 242

QY 111 -----VSGEPHPA-GTPCTESTEGCP 130
DB 243 PPESPRSPSRSPSPATVGTGP--TASDGV 270

RESULT 14
A71905
hypothetical protein jhp0647 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: A71905
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori
A:Reference number: A71905
A:Accession: A71905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <ARN>
A:Cross-references: UNIPROT:Q9ZLD3; GB:AE001497; NID:G4155199; PIDN:AAD0623
C:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0647
C:Superfamily: Helicobacter pylori hypothetical protein HP0708

Query Match 10.1%; Score 71; DB 2; Length 114;
Best Local Similarity 27.2%; Pred. No. 5;
Matches 22; Conservative 20; Mismatches 17; Indels 22; Gaps 4;

QY 50 NSASEGQFC-----IYNNRPNACSYGVAVGVL----AFLTCL----LYLALD 89
DB 6 HSNKERFVRIEDEKKELFAETNENPHGLSMALIGLVFGAFALLVPKLYLSNN 65

QY 90 VYF--POISSVDRKKAVLS 108
DB 66 IYVTSRKINTLEDQKRLLEE 86

RESULT 15
A87697
DegN/DnrJ/BryC1/Strs family protein [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: A87697
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolonitskii, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87697; MUID:21173698; PMID:11259647
A:Accession: A87697
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-386 <STO>
A:Cross-references: UNIPROT:Q9A2F4; GB:AE005673; NID:gl3425359; PIDN:AAK25573.1; GSPDB:C
C:Genetics:
A:Gene: CC3611
C:Superfamily: erythromycin resistance protein

Query Match 10.1%; Score 71; DB 2; Length 386;

Best Local Similarity 26.4%; Pred. No. 18;
Matches 28; Conservative 18; Mismatches 34; Indels 26; Gaps 6;

QY 5 AYGKAGGAGAPP-YTLVRQPHITLRLVSWLFSIVVFGSIYNEGVLNSASGEQFCIYNR 63
DB 70 ANGIGKGDVAFCPSTFAATP-----EVFPVADATPFVDVLPD-----TYNL 112

QY 64 NPNACSYGVAVGVLA--FLTCLLYLALDVY-----PQISSVDRK 102
DB 113 DPAKLEAALA-GVKAEGQLTPKVIADVDFGQPADYPAIKAICDRE 157

RESULT 16
I39792
multidrug-efflux transporter blt - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C:Accession: I39792; D69595
R:Ahmed, M.; Lyass, L.; Markham, P.N.; Taylor, S.S.; Vazquez-Laslop, N.; Neyfakh, A.A. J. Bacteriol. 177, 3904-3910, 1995
A:Title: Two highly similar multidrug transporters of Bacillus subtilis whose expression is induced by tetracycline
A:Reference number: A57353; MUID:95332191; PMID:7608059
A:Accession: I39792
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-400 <RES>
A:Cross-references: UNIPROT:P39843; GB:I32599; NID:G483939; PIDN:AAC36944.1; PID:G483941
R:Kunst, P.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, I.; Koch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadaie, V.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Seguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, E. A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69595
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-400 <KUN>
A:Cross-references: GB:Z99117; GB:AL009126; NID:G2634966; PIDN:CAB14600.1; PID:G2635104
A:Experimental source: strain 168
C:Genetics:
A:Gene: blt
C:Superfamily: tetracycline resistance protein
C:Keywords: antibiotic resistance; transmembrane protein

Query Match 10.1%; Score 71; DB 2; Length 400;
Best Local Similarity 26.6%; Pred. No. 19;
Matches 29; Conservative 20; Mismatches 40; Indels 20; Gaps 4;

QY 26 TILRVVSWLFSIVVFGSIYNEGVLNSASEGE---OFCIYNNRPNACSYGVAVGVLAFL- 80
DB 258 TISSIVAVVQVLLFGKLVNK-----LGEKRMQICLTGAILAFVSTVMSGFLVLL 310

QY 81 -TCLLYLALDVYFPQISSVDRKKAVLSIDIGVSGEPHPAGTPCTESTEG 128
DB 311 VTGFIFLAFDLRLPALT-----AHLNMGAGQGVAGNWSYTSIG 352

RESULT 17
A48959
Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Propionibacterium freudenreichii
C:Species: Propionibacterium freudenreichii
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48959

R;Murakami, K.; Hashimoto, Y.; Murooka, Y.
Appl. Environ. Microbiol. 59, 347-350, 1993
A;Title: Cloning and characterization of the gene encoding glutamate 1-semialdehyde 2,1-
A;Reference number: A48959; MUID:93175878; PMID:8439165
A;Accession: A48959
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 <MUR>
A;Cross-references: UNIPROT:Q06774; GB:D85417; NID:G2347004; PIDN:BAR21914.1; PID:G23470
A;Note: sequence extracted from NCBI backbone (NCBIN:125567, NCBIP:125568)
C;Superfamily: ornithine-oxo-acid aminotransferase
C;Keywords: intramolecular transferase; isomerase

Query Match 10.1%; Score 71; DB 2; Length 441;
Best Local Similarity 29.8%; Pred. No. 21;
Matches 29; Conservative 11; Mismatches 34; Indels 26; Gaps 6;

QY 33 WLFPSVVFSGSVNEG-----YLSNASEGE--QFCIYNRNPNACSYGVAVGV 76
Db 261 WTPDLTFGKVGIGGMPAAVGGSAQLMDYL--APGPPVQAGTLSGNPAACAAGLA--T 316
QY 77 LAFPLTCLLYALDVPYFQISSVKDRKKAVLSDIGVSGEPH 116
Db 317 LALMDAAAYSRLDATADRVSAMAD---AALESAGV---PH 350

RESULT 18
Q0BE6L
glycoprotein H - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 03-Aug-1984 #sequence revision 25-Feb-1985 #text_change 09-Jul-2004
C;Accession: A93065; A36827; A03795; S33046
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: A93065
A;Molecule type: DNA
A;Residues: 1-116 <BAN>
A;Cross-references: UNIPROT:P03231; EMBL:V01555
R;Farrell, P.J.; Barrell, B.G.
Submitted to the EMBL Data Library, June 1984
A;Description: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A38059
A;Accession: A36827
A;Molecule type: DNA
A;Residues: 1-706 <FAR>
A;Cross-references: EMBL:V01555; NID:G59074; PIDN:CAA24797.1; PID:G1334905
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
A;Note: neither amino acid nor nucleotide sequence is given
C;Superfamily: herpesvirus glycoprotein H
C;Keywords: glycoprotein; transmembrane protein
F;60,435,549,604,664/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 71; DB 1; Length 706;
Best Local Similarity 26.4%; Pred. No. 35;
Matches 34; Conservative 23; Mismatches 48; Indels 24; Gaps 7;

QY 2 EGGAYGAGKAGG-----AFDPYTLVRQPHTILRVVSMFLSVFVFGSVINVEGYLSNASE 54
Db 385 KAGVY-SGLIGGATSVLLSAYNRHPLFQLPHTVRETFLTGSHV---LRELRLNVTTQ 439
QY 55 GEQFCIYNRNPN-AS-----YGVAVGVLA--FLTCLLYALDVPYFQISSVKDRKK 103
Db 440 GPNLALYQLLSTALCSALEITGEVLRGLGALGTESGLFSPCYLSRFLDTRDKLSMAP-QE 498
QY 104 AVLSDIGVS 112
Db 499 ATLDAQAVS 507

RESULT 19
A01008
hemolysin, probable NMB2091 [imported] - Neisseria meningitidis (strain MC58 serogroup B).
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: A81008
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rl, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: A81008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <TET>
A;Cross-references: UNIPROT:Q9JXEL; GB:AE002558; GB:AE002098; NID:G7227345; PIDN:AAF42401
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB2091
C;Superfamily: Probable periplasmic protein

Query Match 10.0%; Score 70.5; DB 2; Length 202;
Best Local Similarity 24.5%; Pred. No. 10;
Matches 25; Conservative 20; Mismatches 50; Indels 7; Gaps 3;

QY 23 QPHTILRVVSMFLSVFVFGSVINVEGYLSNASEGEQFCIYNRNPNACSYGVAVGVLAFLTC 82
Db 4 KPHTVRTLIAAIFSLALSGCV--SAVIGSAAVGAKSVDVRRTTGAQTDNDVVALRIETTA 61
QY 83 LLYLALD----VYFPOISSV-KDRKAVLSDIGVSGEPHPAG 119
Db 62 RSYLRQNNQTKYTPQISVGVYNRHLLIGVATGEGERQFVG 103

RESULT 20
C89982
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89982
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89982
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-226 <KUR>
A;Cross-references: UNIPROT:Q99SV6; GB:BA000018; PID:G13701725; PIDN:BAB43018.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SAI1746

Query Match 10.0%; Score 70.5; DB 2; Length 226;
Best Local Similarity 27.8%; Pred. No. 12;
Matches 27; Conservative 20; Mismatches 27; Indels 23; Gaps 5;

QY 14 AFDPYTLVRQ---PH-----TILRVVSMFLSVFVFGSVINVEGYLSNASEGEQFCIYNRP 65
Db 139 AFSQFTELRRVKVPYGIYVFTIILVPFLFSIAIV--LVNYFVLSQSS-----FP 186
QY 66 NACSICVAVGVLAFLTCLLYALDVPYFPOISSVKDRK 102
Db 187 DLYSYTLNIG---FLIISIVILVINYFKQLNKINTRK 220

RESULT 21

T19143
hypothetical protein C09G5.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19143
R;Palmer, S.
submitted to the EMBL Data Library, November 1994
A;Reference number: Z19080
A;Accession: T19143
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-317 <WIL>
A;Cross-references: UNIPROT:Q09456; EMBL:Z46791; PIDN:CRAA6758.1; GSPDB:GN000020; CESP:CO
A;Experimental source: clone C09G5
C;Genetics:
A;Gene: CESP:C09G5.5
A;Map position: 2
A;Introns: 46/3

Query Match 10.0%; Score 70.5; DB 2; Length 317;
Best Local Similarity 19.5%; Pred. No. 17;
Matches 31; Conservative 14; Mismatches 41; Indels 73; Gaps 5;

QY 26 TLIRVSVLFSIVVFGSIVN-----EGYLNASEG----- 55
DB 4 TFLSVAGLSGIVVFGALISVFHYITDINSFVDEAHRELCAFRGVANDAWNSMVNHDSSA 63

QY 56 -----EFCIYNRPNACSYGVAVGLAFLTCLLYLALDVYFPOISSV---KDRKKAFLSD 108
DB 64 RVARSVFVRKQKQSCNCG-----PQASNCAPAGPPGPGCASGD 102

QY 109 IGVSGRPHAPGATP-----CTESTEGCPGP 132
DB 103 RGLDGGQPGPAGKQPGCVAGPAHHQQOECIKCPQAGPG 141

RESULT 22
T33787
hypothetical protein F52F10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33787
R;Graves, T.; Henkhaus, J.; Wohldmann, J.; Bauer, C.; Duckels, G.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid F52F10.
A;Reference number: Z21410
A;Accession: T33787
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-471 <GRA>
A;Cross-references: UNIPROT:Q9UAR0; EMBL:AF101316; PIDN:AAC69232.1; GSPDB:GN000023; CESP:
A;Experimental source: strain Bristol N2; clone F52F10
C;Genetics:
A;Gene: CESP:F52F10.2
A;Map position: 5
A;Introns: 39/1; 122/2; 203/1; 261/1; 308/2; 355/2; 448/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C25E10.3

Query Match 10.0%; Score 70.5; DB 2; Length 471;
Best Local Similarity 27.4%; Pred. No. 25;
Matches 32; Conservative 15; Mismatches 35; Indels 35; Gaps 7;

QY 19 TLVRQPHITLRVSWLFSIVVFGS--IWNEGYLNASEGEQFCIYNRPNA----- 67
DB 354 TIV-QPRFI-----YLFSSISLFTLYIVTPY---KSGIVEVAMYNATDNTGCDPDKYSW 404

QY 68 CSYGVANGVLAFLTCLLY-----LALDVYFPOI-----SSVKDRKKAFLSDI 109
DB 405 CEGGIAPQPIFLCLCCVFGVFGMTWPSSAISLDTIYSKILGNIDQSVMQGAAILDDI 461

RESULT 23
F90291
hypothetical protein SSO1353 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: F90291
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90291
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-663 <KUR>
A;Cross-references: UNIPROT:Q97YG8; GB:AE006641; NID:g13814563; PIDN:AAK41589.1; GSPDB:G
C;Genetics:
A;Gene: SSO1353
C;Superfamily: beta-glucosidase, GBA2 type

Query Match 10.0%; Score 70.5; DB 2; Length 663;
Best Local Similarity 27.6%; Pred. No. 36;
Matches 32; Conservative 16; Mismatches 47; Indels 21; Gaps 8;

QY 25 HTILRVSWLFSIVVFGSIVNFGYLNASAS----EGEQFCIYNRPNACSYGVAVGLAFL 80
DB 299 HNVVNVKWLGD-----AIINSAYILSSNTWLDEKGRFAIYEA-PONCPYLGTIG----- 347

QY 81 TCLLYLALDV--YFPOISSVKDRKKAFLSDIGVSG-EHPHAPGTPCTES-TEGCPGP 132
DB 348 ACYFEGSLPVLMPFELE--KSFLLKLLIRHIREDGIVPHDLGYHSLDSIDTGTSP 401

RESULT 24
SAVIME
large surface antigen - duck hepatitis virus (strain China)
N;Contains: major surface antigen; middle surface antigen
C;Species: duck hepatitis virus, DHV
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S12842
R;Tong, S.; Matthes, F.; Teubner, K.; Blum, H.E.
Nucleic Acids Res. 18, 6139, 1990
A;Title: Complete nucleotide sequence of a Chinese duck hepatitis B virus.
A;Reference number: S12840; MUID:91045091; PMID:2235506
A;Accession: S12842
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-365 <TON>
A;Cross-references: UNIPROT:P30029; GB:M21953; NID:g325435; PIDN:AAA45746.1; PID:g325438
C;Genetics:
A;Gene: pre-S1/pre-S2/S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen (gene pre-S2/S) #status predicted <DSA>
F;89-365/Product: middle surface antigen (gene S) #status predicted <MSA>
F;199-365/Product: major surface antigen (gene S) #status predicted <MSA>
F;297/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.0%; Score 70; DB 1; Length 365;
Best Local Similarity 27.5%; Pred. No. 22;
Matches 19; Conservative 9; Mismatches 29; Indels 12; Gaps 2;

QY 71 GVAVGVLAFITCLLYL-----ALDVYFPOISSVKDRKKAFLSDIGVSGEHPHAGTPC 122
DB 205 GILAGLIGLVSPFLIKILEILRLKLDWWISLSSPKGMQCAFDQTGAQISPHYAGS-- 262

QY 123 TESTEGCPG 131
DB 263 --CPWGPCG 269

RESULT 25
AH3095
nitric oxide reductase, cytochrome b subunit norB [imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
R:Accession: AH3095
R:Wood, D.W.; Sebval, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH3095
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-448 <KUR>
A:Cross-references: UNIPROT:Q8U7R1; GB:AE008689; PIDN:AAL45182.1; PID:gl17742859; GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: norB
A:Map position: linear chromosome

Query Match 10.0%; Score 70; DB 2; Length 448;
Best Local Similarity 23.0%; Pred. No. 27;
Matches 28; Conservative 13; Mismatches 35; Indels 46; Gaps 4;

QY 17 PYTLVRQPHILRVV-----SWLFSIWFSGIYN 45
| : : : : : ||
| : : : : : ||
Db 45 PFNIVRMHTNALVWLLMGFMGSGTYLLPEETETELYSFKLAIAQFWIFLVAANA VAVV- 103
| : : : : : ||
QY 46 EGYLSASGEQFCIYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKORKKAV 105
| : : : : : ||
| : : : : : ||
Db 104 -GYMFRHIEGREFL---EQPFAIKVGIVLWLMFLFNITWTAL-----KGRKTTV 149
| : : : : : ||
QY 106 LS 107
| : : : : : ||
Db 150 IN 151

RESULT 26
B98191
nitric oxide reductase cytochrome b chain (AJ298324) [imported] - Agrobacterium tumefaci
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
R:Accession: B98191
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-448 <KUR>
A:Cross-references: UNIPROT:Q8U7R1; GB:AE007870; PIDN:AAK89052.1; PID:gl5158847; GSPDB:C
C:Genetics:
A:Gene: AGR L 956
A:Map position: linear chromosome

Query Match 10.0%; Score 70; DB 2; Length 448;
Best Local Similarity 23.0%; Pred. No. 27;
Matches 28; Conservative 13; Mismatches 35; Indels 46; Gaps 4;

QY 17 PYTLVRQPHILRVV-----SWLFSIWFSGIYN 45
| : : : : : ||
| : : : : : ||
Db 45 PFNIVRMHTNALVWLLMGFMGSGTYLLPEETETELYSFKLAIAQFWIFLVAANA VAVV- 103
| : : : : : ||
QY 46 EGYLSASGEQFCIYNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKORKKAV 105
| : : : : : ||
| : : : : : ||
Db 104 -GYMFRHIEGREFL---EQPFAIKVGIVLWLMFLFNITWTAL-----KGRKTTV 149
| : : : : : ||
QY 106 LS 107
| : : : : : ||
Db 150 IN 151

RESULT 27

H90010
PRS system, mannitol specific IIBC component [imported] - Staphylococcus aureus (strain I
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R:Accession: H90010
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <KUR>
A:Cross-references: UNIPROT:Q99SA3; GB:BA000018; PID:gl3701957; PIDN:BAB43249.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: mtlP
C:Superfamily: phosphotransferase system mannitol-specific enzyme II factor II; phosphot

Query Match 10.0%; Score 70; DB 2; Length 512;
Best Local Similarity 26.8%; Pred. No. 31;
Matches 42; Conservative 23; Mismatches 54; Indels 38; Gaps 10;

QY 5 AVGAG---KAGAFDPYTLVRQPHILRVVSWLFSIWFSGIYN-----GYLNSAS 53
| : : : : : ||
| : : : : : ||
Db 249 SYGAGIIHFLGGIHIYF---PYVLMRPL--LFTAVILGGMGTGVTATQATGFGKSPAS 302
| : : : : : ||
| : : : : : ||
QY 54 EGEQFCIYNRN--PNACSYGVAVGV--LAFLTCLLYLALDVYF-----POISSVK 99
| : : : : : ||
| : : : : : ||
Db 303 PG-SFIVYCLNAPRGFEFLHMLGVFLAALVSFVVAALIMKFTREPQDLAAQAQMENTK 361
| : : : : : ||
| : : : : : ||
QY 100 DRK-----KAVLSDIGVSGEHPAGTPC--TESTEGCP 130
| : : : : : ||
| : : : : : ||
Db 362 GKSSVASKLVSSDKNVNTENASGNVSETSSDDDP 398

RESULT 28

A46227
voltage-dependent Ca2+ channel alpha 1-subunit - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 27-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R:Yaney, G.C.; Wheeler, M.B.; Wei, X.; Perez-Reyes, E.; Birnbaumer, L.; Boyd III, A.E.; N
Mol. Endocrinol. 6, 2143-2152, 1992
A:Title: Cloning of a novel alpha 1-subunit of the voltage-dependent calcium channel from
A:Reference number: A46227; MUID:93149124; PMID:1337146
A:Accession: A46227
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1610 <YAN>
A:Cross-references: UNIPROT:Q99244
A:Experimental source: insulin-secreting cell line HIT-T15
A>Note: sequence extracted from NCBI backbone (NCBI:P123692)
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 10.0%; Score 70; DB 2; Length 1610;
Best Local Similarity 25.5%; Pred. No. 1.1e+02;
Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYGAGKAGAFDPYTL-----VRQPHITLRVSWLFSIWFSGIYNVSGEYNSASGEQ 57
| : : : : : ||
| : : : : : ||
Db 221 EGGNHSSGKSGG--FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 262
| : : : : : ||
| : : : : : ||
QY 58 FCIYNRNPNACSYGVAVGVLAFLTCLLYLALDVYF-----QISSVKDKKAVLSD 108
| : : : : : ||
| : : : : : ||
Db 263 -----IIKAWPLHLIALVLVFLVIIYAIIGLELFIGKWHKTCFFAD 304
| : : : : : ||
| : : : : : ||
QY 109 IGVSGEHPAGTPC-----TESTEGCPG 132
| : : : : : ||
| : : : : : ||

Db 305 SDIAVEDPA--PCAFSGNGRQCAVNGTECRSGWGP 339

RESULT 29

JH0422

A;Molecule type: mRNA

A;Residues: 1-1646 <HUI>

A;Cross-references: GB:M76582; NID:G206573; PIDN:AAA2015.1; PID:G206574

A;Experimental source: brain

R;Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Lester, H.A.; Davidson, N.

Proc. Natl. Acad. Sci. U.S.A. 87, 3391-3395, 1990

A;Title: Rat brain expresses a heterogeneous family of calcium channels.

A;Reference number: A35901; MUID:90239020; PMID:1692134

A;Accession: D35901

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A;Molecule type: mRNA

A;Residues: 1247-1434 <SNU>

A;Experimental source: brain

R;Yu, A.S.L.; Hebert, S.C.; Brenner, B.M.; Lytton, J.

Proc. Natl. Acad. Sci. U.S.A. 89, 10494-10498, 1992

A;Title: Molecular characterization and nephron distribution of a family of transcripts

A;Reference number: A46422; MUID:93066265; PMID:1279681

A;Accession: I60901

A;Status: preliminary; translated from GB/ENBL/DBJ

A;Molecule type: mRNA

A;Residues: 1040-1261,1305-1365 <RES>

A;Cross-references: GB:M99221; NID:G203370; PIDN:AAA40895.1; PID:G203371

A;Experimental source: kidney

C;Comment: Calcium channels are essential for many cellular functions, such as muscle co

n.

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Keywords: alternative splicing; calcium binding; calcium channel; glycoprotein; phosph

F;1463-1491/Domain: calcium binding #status predicted <BFC>

F;154,224,328/Binding site: carboxylate (Asn) (covalent) #status predicted

F;464,848,1489,1584/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 10.0%; Score 70; DB 2; Length 1646;

Best Local Similarity 25.5%; Pred. No. 1.1e+02;

Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYGAGKAGGAPDPYTL-----VRPHITLRVSVWLFVFGSIVNEGYNLSASGEQ 57

Db 221 EGGHSSGKSGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 262

QY 58 FCYINRNPNACSGVAVGVLAFLTCLLYLALDVFP-----QISSVKDRKKAVALSD 108

Db 263 -----IIKAMPVLLHIALLVFVIIIAIIGLELFIGKMKTCFFAD 304

QY 109 IGVSGBPHPAGTGPC-----TESTEGCPGP 132

Db 305 SDIAVEDPA--PCAFSGNGRQCAVNGTECRSGWGP 339

RESULT 30

JH0564

A;Molecule type: mRNA

A;Residues: 1-2181 <SEI>

A;Cross-references: GB:M83566; NID:G179751; PIDN:AAA35629.1; PID:G179752

A;Experimental source: pancreatic beta cells

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Keywords: membrane protein; voltage-gated ion channel

C;Accession: JH0564

R;Williams, M.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi, G.; Ellis, S.B.;

Neuron 8, 71-84, 1992

A;Title: Structure and functional expression of alphas, alpha2, and beta subunits of a n

A;Reference number: JH0564; MUID:92110010; PMID:1309651

A;Accession: JH0564

A;Molecule type: mRNA

A;Residues: 1-2161 <WIL>

A;Cross-references: GB:M76558

A;Experimental source: neuroblastoma, cell line IMR32

C;Comment: This protein is a subunit of the voltage-dependent calcium channel.

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Keywords: transmembrane protein

F;127-145/Domain: transmembrane #status predicted <IS1>

F;164-183/Domain: transmembrane #status predicted <IS2>

F;195-214/Domain: transmembrane #status predicted <IS3>

F;236-254/Domain: transmembrane #status predicted <IS4>

F;274-293/Domain: transmembrane #status predicted <IS5>

F;382-406/Domain: transmembrane #status predicted <IS6>

F;524-542/Domain: transmembrane #status predicted <I11>

F;558-577/Domain: transmembrane #status predicted <I12>

F;586-603/Domain: transmembrane #status predicted <I13>

F;615-633/Domain: transmembrane #status predicted <I14>

F;653-672/Domain: transmembrane #status predicted <I15>

F;728-752/Domain: transmembrane #status predicted <I16>

F;888-905/Domain: transmembrane #status predicted <S11>

F;922-941/Domain: transmembrane #status predicted <S21>

F;954-972/Domain: transmembrane #status predicted <S31>

F;980-998/Domain: transmembrane #status predicted <S41>

F;1018-1037/Domain: transmembrane #status predicted <S51>

F;1128-1152/Domain: transmembrane #status predicted <S61>

F;1206-1224/Domain: transmembrane #status predicted <VS1>

F;1240-1259/Domain: transmembrane #status predicted <VS2>

F;1268-1286/Domain: transmembrane #status predicted <VS3>

F;1315-1333/Domain: transmembrane #status predicted <VS4>

F;1353-1372/Domain: transmembrane #status predicted <VS5>

F;1440-1464/Domain: transmembrane #status predicted <VS6>

Query Match 10.0%; Score 70; DB 2; Length 2161;

Best Local Similarity 25.5%; Pred. No. 1.4e+02;

Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYGAGKAGGAPDPYTL-----VRPHITLRVSVWLFVFGSIVNEGYNLSASGEQ 57

Db 222 EGGHSSGKSGG-FDVKALRAFRVLRP---LRLVSGVPSLQV-----VLNS----- 263

QY 58 FCYINRNPNACSGVAVGVLAFLTCLLYLALDVFP-----QISSVKDRKKAVALSD 108

Db 264 -----IIKAMPVLLHIALLVFVIIIAIIGLELFIGKMKTCFFAD 305

QY 109 IGVSGBPHPAGTGPC-----TESTEGCPGP 132

Db 306 SDIAVEDPA--PCAFSGNGRQCAVNGTECRSGWGP 340

RESULT 31

A38198

A;Molecule type: mRNA

A;Residues: 1-2181 <SEI>

A;Cross-references: GB:M83566; NID:G179751; PIDN:AAA35629.1; PID:G179752

A;Experimental source: pancreatic beta cells

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Keywords: membrane protein; voltage-gated ion channel

C;Accession: A38198

R;Seino, S.; Chen, L.; Seino, M.; Blondel, O.; Takeda, J.; Johnson, J.H.; Bell, G.I.

Proc. Natl. Acad. Sci. U.S.A. 89, 584-588, 1992

A;Title: Cloning of the alpha 1 subunit of a voltage-dependent calcium channel expressed

A;Reference number: A38198; MUID:92115705; PMID:1309948

A;Accession: A38198

A;Molecule type: mRNA

A;Residues: 1-2181 <SEI>

A;Cross-references: GB:M83566; NID:G179751; PIDN:AAA35629.1; PID:G179752

A;Experimental source: pancreatic beta cells

C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

C;Keywords: membrane protein; voltage-gated ion channel

Query Match 10.0%; Score 70; DB 2; Length 2181;

Best Local Similarity 25.5%; Pred. No. 1.5e+02;

Matches 40; Conservative 16; Mismatches 37; Indels 64; Gaps 8;

QY 2 EGGAYGAGKAGGAPDPYTL-----VRPHITLRVSVWLFVFGSIVNEGYNLSASGEQ 57

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: AB2035; MUID: 20406833; PMID: 10952301

A;Molecule type: DNA

A;Cross-references: UNIPROT:Q9KJPJ4; GB:AE004307; GB:AE003852; NID:g9656934; PIDN:AAF9551

C;Genetics:

A;Map position: 1

C;Keywords: 3Fe-4S; metalloprotein; oxidoreductase

F;37-1530/Product: glutamate synthase #status predicted <MA1>
E:37/active site: Cys #status predicted

F; 1149, 1155, 1160/Binding site: 3FE-4S cluster (Cys) (covariant) #status predicted

Query Match	9.9%	Score 83.3, DB 2, Length 1000
Best [local] Similarity	28.0%	Pred. No. 1.1e+02:

[illegible][illegible]

100

$\frac{1}{2}$

RESULT 38

halorhodopsin - Halobacteriaceae gen. sp. (fragment)

```
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
```

R;Otomo, J.; Tomioka, H.; Sasabe, H.
Nucleic Acids 1112 7-12 1992

A;title: Properties and the primary structure of a new harpacticoid
A;reference number: A56808: PMID:1420272

A;ACCESSION: A56808
 A-STATUS: preliminary

A: Molecule type: DNA
A: Residue: 25-239 <OT1>

A:Experimental source: strain mex
A:Note: sequence extracted from NCBI backbone (NCBIN:118503, NCBIIP:118504)

A:Status: preliminary

A;Residues: 1-29 <OTO>

C; Keywords: photoreceptor; transmembrane protein

Query Match 9.8%; Score 69; DB 2; Length 239;

Matches 27; Conservative 17; Mismatches 42; Indels 32; Gaps 4;

QY 7 GAGKAGGAFDPYTLVRQPHITLRVSVLFSIVWFGSIVNEGVLNSASEGEQFCIYNRNP 66

Db
89 GAGPEGGVFTPWG-----RYLTWAFSTPMI--LIAGLLAGSNMSKLFIAVVADVG 137

QY 67 ACSYGVAGV-----LAFITCLLYLALDVYFPQISSVNDKKNVLSDI I09

DD 138 MCIIGLAAALITSSYLLRWVWIGISCAFFVVDITLDAEN-----ANDAEVAGIADI 100

RESULT 39

F97790 putrescine-ornithine antiporter [imported] - Rickettsia conorii (strain Malish 7)

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97790
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
C;Accession: F97790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <KUR>
A;Cross-references: UNIPROT:Q92HP5; GB:AE006914; PIDN:AAL03264.1; PID:G15619819; GSPDB:G
C;Genetic: 1
A;Gene: potE
C;Superfamily: L-lysine transport protein

Query Match 9.8%; Score 69; DB 2; Length 427;
Best Local Similarity 26.8%; Pred. No. 32;
Matches 22; Conservative 14; Mismatches 32; Indels 14; Gaps 2;

QY 33 WLFSLFVFGSVINVEGLNS-----ASEG--EQFCIYNRPNACSYGVAVGLA 78
Db 267 WSSVITVIAIICIGTLNWLVTSGQIALGLABDGLLPKFFAKNSNNAPTHGIIVSCIG 326

QY 79 FLTCLLYLALDVVFPQISSVKD 100
Db 327 IVPLLVFTANDNFAKQITQIID 348

RESULT 40
T02450
probable cytochrome P450 F4I18.5 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02450; B84897
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence.
A;Reference number: Z14674
A;Accession: T02450
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-537 <RQU>
A;Cross-references: UNIPROT:O80823; EMBL:AC004665; NID:g3386593; PID:g3386598
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84897
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-537 <STO>
A;Cross-references: GB:AE002093; NID:g6598466; PIDN:AAC62873.2; GSPDB:GN00139
C;Genetics:
A;Gene: At2g45970; F4I18.5
A;Map position: 2
C;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology
F;302-480/Domain: cytochrome P450 homology <P45>

Query Match 9.8%; Score 69; DB 2; Length 537;
Best Local Similarity 24.8%; Pred. No. 41;
Matches 25; Conservative 17; Mismatches 47; Indels 12; Gaps 4;

QY 31 VSMFLSVFVFGSVINVEGLNS-----ASEGFCIYNRPNACSYGVAVGLAFITCLL 84
Db 314 LSWFFWLITQHPAIEDKILREICTVLIVTRGDDVALVTEPLDSE---ELDRVLFLKAL 370

QY 85 YLALDVYFFQISSVKORKKAVLSDIGVSGEPHPAGTPTCTES 125
Db 371 SETRLY-PSVP--EDSKRAVKDVLDPDGTFFVAGSSITVS 408

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B84731
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-163 <STO>
A;Cross-references: UNIPROT:Q92V57; GB:AE002093; NID:g3831471; PIDN:AAC69953.1; GSPDB:GN
C;Genetic: 1
A;Gene: At2g32280
A;Map position: 2

Query Match 9.7%; Score 68.5; DB 2; Length 163;
Best Local Similarity 30.3%; Pred. No. 13;
Matches 27; Conservative 12; Mismatches 41; Indels 9; Gaps 4;

QY 15 FDPYTLVRQPHITLRVSVWLFSLVFGSVINVEGLNSASEGEQFCIYNRPNACSYGVAV 74
Db 84 FORSSSTRQISMACILVLTWIVFAVGFGSIVGTMSNKSRS--CGFTHH-HFLSIG--- 137

QY 75 GVLAFITCLLYLALDVVFPQISSVKDRKK 103
Db 138 GLICFHALFCVA---YVSATAAKDEAK 163

RESULT 42
MFTV2C
matrix protein M2 - influenza B virus (strain B/Ann Arbor/1/66 [cold-adapted])
C;Species: Influenza B virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: B30064
R;DeBorde, D.C.; Donabedian, A.M.; Herlocher, M.L.; Naeve, C.W.; Maassab, H.F. Virology 163, 429-443, 1988
A;Title: Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66 influenza vi
A;Reference number: A28604; MUID:88179548; PMID:3354202
A;Accession: B30064
A;Molecule type: genomic RNA
A;Residues: 1-195 <DEB>
A;Cross-references: UNIPROT:P13881
C;Comment: The RNA sequence was obtained from GenBank, release 58.0.
C;Genetics:
A;Map position: segment 7
C;Superfamily: influenza virus matrix protein M2
C;Keywords: matrix protein

Query Match 9.7%; Score 68.5; DB 1; Length 195;
Best Local Similarity 28.2%; Pred. No. 16;
Matches 31; Conservative 15; Mismatches 47; Indels 17; Gaps 5;

QY 4 GAYGAGKAG--GAF--DPYTLVRQPHITLRVSVWLFSLVFGSVINVEGLNSASEGEQF 58
Db 65 GNGSAKALYKGFSSCEIPIMLEPFQILSLCSFILSAHF--MAWTGHLNQIKRGVNL 123

QY 59 CIYNRPNACSYGVAVGLAFITCLLYLALDVYFFQISSVKDRKKAVLSD 108
Db 124 KIRIRPNKETINREVSIILR-----HSYQKEIOA-KETMKVLSLD 162

RESULT 43
MFTV2W
matrix protein M2 - influenza B virus (strain B/Ann Arbor/1/66 [wild-type])
C;Species: Influenza B virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

C;Accession: D30064
R;DeBorde, D.C.; Donabedian, A.M.; Herlocher, M.L.; Naeve, C.W.; Maaseab, H.F.
Virology 163, 429-443, 1988
A;Title: Sequence comparison of wild-type and cold-adapted B/Ann Arbor/1/66 influenza vi
A;Reference number: A28604; MUID:88179548; PMID:3354202
A;Accession: D30064
A;Molecule type: genomic RNA
A;Residues: 1-195 <DEB>
A;Cross-references: UNIPROT:P13882
C;Comment: The RNA sequence was obtained from GenBank, release 58.0.
C;Genetics:
A;Map position: segment 7
C;Superfamily: influenza virus matrix protein M2
C;Keywords: matrix protein

Query Match 9.7%; Score 68.5; DB 1; Length 195;
Best Local Similarity 28.2%; Pred. No. 16;
Matches 31; Conservative 15; Mismatches 47; Indels 17; Gaps 5;

QY 4 GAYGAGKAG--GAF---DPYTLVRQPHITLRVSWLFSIVVFGSIVNMGYNSASGEQF 58
DB 65 GCNGSAKAEYLGKFSCEETPIMLEPQILSICFSLALHF-MAWTIGHLNQIKRGVNL 123

QY 59 CIYRNPNACSYGAVGVLAFLTCLLYLALDVYFPQISSVKRKAVALSD 108
DB 124 KIRIRPNKETINREVSILR-----HSYQKEIQ-A-KETMKEVLSD 162

RESULT 44
MFIVB2
matrix protein M2 - influenza B virus (strain B/Singapore/222/79)
C;Species: influenza B virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: B25619
R;Hiebert, S.W.; Williams, M.A.; Lamb, R.A.
Virology 155, 747-751, 1986
A;Title: Nucleotide sequence of RNA segment 7 of influenza B/Singapore/222/79: maintenar
A;Reference number: A94351; MUID:87071690; PMID:3788064
A;Accession: B25619
A;Molecule type: mRNA
A;Residues: 1-195 <HIE>
A;Cross-references: UNIPROT:P08383
A;Note: the authors translated the codon CAT for residue 195 as Gln
C;Comment: The RNA sequence was obtained from GenBank, release 52.0.
C;Genetics:
A;Map position: segment 7
C;Superfamily: influenza virus matrix protein M2
C;Keywords: matrix protein

Query Match 9.7%; Score 68.5; DB 1; Length 195;
Best Local Similarity 28.2%; Pred. No. 16;
Matches 31; Conservative 15; Mismatches 47; Indels 17; Gaps 5;

QY 4 GAYGAGKAG--GAF---DPYTLVRQPHITLRVSWLFSIVVFGSIVNMGYNSASGEQF 58
DB 65 GCNGSAKAEYLGKFSCEETPIMLEPQILSICFSLALHF-MAWTIGHLNQIKRGVNL 123

QY 59 CIYRNPNACSYGAVGVLAFLTCLLYLALDVYFPQISSVKRKAVALSD 108
DB 124 KIRIRPNKETINREVSILR-----HSYQKEIQ-A-KETMKEVLSD 162

RESULT 45
C83964
cation-transporting ATPase pacL [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83964
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83964

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-902 <STO>
A;Cross-references: UNIPROT:Q9KX9; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BA062;
A;Experimental source: strain C-125
C;Genetics:
A;Gene: pacL
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain 1

Query Match 9.7%; Score 68.5; DB 2; Length 902;
Best Local Similarity 25.0%; Pred. No. 81;
Matches 20; Conservative 17; Mismatches 34; Indels 9; Gaps 2;

QY 19 TLVRQPHITLRVSWLFSIVVFGSIVNMGYNSASGEQFCIYRNPNACSYGAVGVLA 78
DB 798 TLQANPDDLTRAQSVAFVTLVMAQLIHVPDCRS-----EYSVFHRNPFENKY----LVLA 848

QY 79 FLTCLLYLALDVYFPQISSV 98
DB 849 VLSSVLLMLIVYPPLOQV 868

RESULT 46
CGCH2S
collagen alpha 2(I) chain precursor - chicken (fragments)
C;Species: Gallus gallus (chicken)
C;Date: 24-Apr-1984 #sequence_revision 15-Aug-1997 #text_change 09-Jul-2004
C;Accession: I50206; I50207; S07354; S10848; S10480; S11146; I50628; I50170; I50625; I506
R;Boedtker, H.; Finer, M.; Aho, S.
Ann. N. Y. Acad. Sci. 460, 85-116, 1985
A;Title: The structure of the chicken alpha 2 collagen gene.
A;Reference number: I50206; MUID:86185168; PMID:3868961
A;Accession: I50206
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-245 <BOE>
A;Cross-references: UNIPROT:P02467; GB:M25963; NID:g211581; PIDN:AAA69960.1; PID:g211605
A;Accession: I50207
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 246-431 <BO2>
A;Cross-references: GB:M25965; NID:g211583; PIDN:AAA69961.1; PID:g211606
R;Aho, S.; Tate, V.; Boedtker, H.
Nucleic Acids Res. 12, 6117-6125, 1984
A;Title: Location of the 11 bp exon in the chicken pro alpha-2(I) collagen gene.
A;Reference number: S07354; MUID:84297217; PMID:6473103
A;Accession: S07354
A;Molecule type: DNA
A;Residues: 1-33 <AHO>
A;Cross-references: EMBL:X00760; NID:g63266; PIDN:CAA25330.1; PID:g63267
R;Tate, V.E.; Finer, M.H.; Boedtker, H.; Doty, P.
Nucleic Acids Res. 11, 91-104, 1983
A;Title: Chick pro-alpha-2 (I) collagen gene: exon location and coding potential for the
A;Reference number: S10480; MUID:83246518; PMID:6135195
A;Accession: S10848
A;Molecule type: mRNA
A;Residues: 1-89 <TAT>
A;Cross-references: EMBL:X02657; NID:g63314; PIDN:CAA26493.1; PID:g63315
A;Accession: S10480
A;Molecule type: DNA
A;Residues: 17-73 <TAW>
R;Vogeli, G.; Ohkubo, H.; Sobel, M.E.; Yamada, Y.; Pastan, I.; de Crombrughe, B.
Proc. Natl. Acad. Sci. U.S.A. 78, 5334-5338, 1981
A;Title: Structure of the promoter for chicken alpha-2 type I collagen gene.
A;Reference number: S11146; MUID:82060240; PMID:6946474
A;Accession: S11146
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <VOG>
A;Cross-references: EMBL:J00821
R;Yamada, Y.; Avvedimento, V.E.; Mudryj, M.; Ohkubo, H.; Vogeli, G.; Irani, M.; Pastan,
Cell 22, 887-892, 1980

A;Title: The collagen gene: evidence for its evolutionary assembly by amplification of a
A;Reference number: I50170; MUID:81112157; PMID:7460017
A;Accession: I50628
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 126-161 <YAM>
A;Cross-references: EMBL:V00400; NID:G63305; PID:G833611
A;Accession: I50170
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 126-161 <YAZ>
A;Cross-references: GB:J00828; NID:G211295; PIDN:AAA51612.1; PID:G211317
A;Accession: I50625
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 530-558 <YAZ>
A;Cross-references: EMBL:V00396; NID:G63295; PID:G833609
A;Accession: I50626
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 572-601 <YAA>
A;Cross-references: EMBL:V00398; NID:G632299; PID:G833610
A;Accession: I50624
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 433-483 <YAS>
A;Cross-references: EMBL:V00394; NID:G632287; PID:G833608
R;Kang, A.H.; Gross, J.
Biochemistry 9, 796-804, 1970
A;Title: Amino acid sequence of cyanogen bromide peptides from the amino-terminal region
A;Reference number: A90568; MUID:70131186; PMID:4313735
A;Accession: A90568
A;Molecule type: protein
A;Residues: 'Z', 79-92 <KAN>
A;Experimental source: skin
R;Kang, A.H.; Igarashi, S.; Gross, J.
Biochemistry 8, 3200-3204, 1969
A;Title: Characterization of the cyanogen bromide peptides from the alpha2 chain of chick
A;Reference number: A90557; MUID:69285369; PMID:5809220
A;Accession: A90557
A;Molecule type: protein
A;Residues: 'Z', 79-95; 398-409, 'A', 411, 'V', 413-428 <KAZ>
A;Experimental source: skin
A;Note: the compositions of the six CNBr peptides were determined. CNBr0 is residues 93-
R;Higberger, J.H.; Kang, A.H.; Gross, J.
Biochemistry 10, 610-616, 1971
A;Title: Comparative studies on the amino acid sequence of the alpha2-CB2 peptides from
A;Reference number: A90358; MUID:71115216; PMID:5544653
A;Accession: B90358
A;Molecule type: protein
A;Residues: 399-409, 'A', 411, 'V', 413-428 <HIG>
A;Experimental source: skin
R;Lane, J.M.; Miller, E.J.
Biochemistry 8, 2134-2139, 1969
A;Title: Isolation and characterization of the peptides derived from the alpha2 chain of
A;Reference number: A90555; MUID:69206882; PMID:5785233
A;Accession: A90555
A;Molecule type: protein
A;Residues: 'Z', 79-95; 398-409, 'A', 411, 'V', 413-428 <LAN>
A;Experimental source: bone
A;Note: the compositions of the six CNBr peptides were determined
A;Note: the compositions of CNBr1, CNBr0, and CNBr2 are identical with those from skin a
R;Igarashi, S.; Kang, A.H.; Gross, J.
Biochem. Biophys. Res. Commun. 38, 697-702, 1970
A;Title: Renaturation and ordering by electron microscopy of the cyanogen bromide peptid
A;Reference number: A90168; MUID:70181851; PMID:5443711
A;Contents: annotation; skin, order of CNBr peptides
R;Vuust, J.; Lane, J.M.; Pietrek, P.P.; Miller, E.J.; Piez, K.A.
Biochem. Biophys. Res. Commun. 38, 703-708, 1970
A;Title: The order of the CNBr peptides from the alpha2 chain of collagen.
A;Reference number: A90169; MUID:70181852; PMID:5443712
A;Contents: annotation; bone, order of CNBr peptides
R;Wozney, J.; Hanahan, D.; Tate, V.; Boedtker, H.; Doty, P.

Nature 294, 129-135, 1981
A;Title: Structure of the pro alpha-2(I) collagen gene.
A;Reference number: S07327; MUID:82058081; PMID:6272119
A;Accession: S07327
A;Molecule type: DNA
A;Residues: 74-92; 93, 247-431; 432, 693-774 <WOZ>
A;Cross-references: EMBL:J00826
R;Fuller, F.; Boedtker, H.
Biochemistry 20, 996-1006, 1981
A;Title: Sequence determination and analysis of the 3' region of chicken pro-alpha 1(I) c
A;Reference number: I50623; MUID:81160715; PMID:6927845
A;Accession: I50623
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 506-830, 'T', 831-903, 'N', 904-964 <FUL>
A;Cross-references: EMBL:V00390; NID:G63248; PIDN:CAA23688.1; PID:G63249
R;Avvedimento, E.V.; Vogeli, G.; Yamada, Y.; Maizel, J.V.
Cell 21, 689-696, 1980
A;Title: Correlation between splicing sites within an intron and their sequence complemer
A;Reference number: I50172; MUID:81064671; PMID:6159982
A;Accession: I50172
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-558 <AVV>
A;Cross-references: GB:M10581; NID:G211323; PIDN:AAA48637.1; PID:G211326
R;Lehrach, H.; Frischauf, A.M.; Hanahan, D.; Wozney, J.; Fuller, F.; Crkvenjakov, R.; Bo
Proc. Natl. Acad. Sci. U.S.A. 75, 5417-5421, 1978
A;Title: Construction and characterization of a 2.5-kilobase procollagen clone.
A;Reference number: I50171; MUID:79074829; PMID:364479
A;Accession: I50171
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 484-505 <LEH>
A;Cross-references: GB:J00837; NID:G4530617; PIDN:AAA51614.1; PID:G211320
C;Genetics:
A;Gene: COL1A2
A;Introns: 24/1; 27/3; 33/3; 45/3; 73/3; 92/3; 107/3; 125/3; 143/3; 161/3; 179/3; 197/3;
A;Note: the list of introns is incomplete
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: blocked amino end; coiled coil; extracellular matrix; glycoprotein; hydroxyp
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-77/Domain: amino-terminal propeptide #status predicted <PRO>
F;78-94/Product: collagen alpha 2(I) chain (fragments) #status predicted <MATN>
F;78-96/Region: amino-terminal nonhelical telopeptide
F;737-964/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F;78/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidone carbo
F;83/Modified site: allysine (Lys) #status experimental
F;422,425/Modified site: 4-hydroxyproline (Pro) #status experimental
F;866/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 9.7%; Score 68.5; DB 1; Length 964;
Best Local Similarity 31.6%; Pred. No. 87;
Matches 18; Conservative 6; Mismatches 30; Indels 3; Gaps 1;
QY 76 VLAFITCLLYALDVVFPQISSVKDRKAVLSDIGVSGFHPAGTPTCTESTGCGCP 132
DB 9 IULLLVATSYLTSQH---VSEASAGRKGRGKGGPPGPPGPPGPPGPPGPPG 62
RESULT 47
B71635
phosphatidylglycerophosphatase A (pgpa) RP750 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichert-Ponten, T.; Alsmark, U.
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: B71635
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-201 <AND>

A:Gene: GDB:COL9A2
A:Cross-references: GDB:138310; OMIM:120260
A:Map position: lp33-lp32.2
A:Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(IX) chain, and one alpha 3(IX) chain.
C:Function:
A:Description: structural component of extracellular fibrous polymer associated with type IX collagen.
C:Keywords: chondroitin sulfate proteoglycan; coiled coil; extracellular matrix; glycoprotein
F:1-114/Domain: collagenous COL3 (fragment) #status predicted <COL3>
F:115-131/Domain: non-collagenous NC3 #status predicted <NC3>
F:132-470/Domain: collagenous COL2 #status predicted <COL2>
F:471-500/Domain: non-collagenous NC2 #status predicted <NC2>
F:501-615/Domain: collagenous COL1 #status predicted <COL1>
F:616-618/Domain: non-collagenous NC1 (fragment) #status predicted <NC1>

F:120/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 9.7%; Score 68; DB 2; Length 618;
Best Local Similarity 35.7%; Pred. NO. 61;
Matches 15; Conservative 5; Mismatches 20; Indels 2; Gaps 1;

QY 93 POISSVKDR--KKAVLSDIGVSGEPHPAGTPCTESTEGCGGP 132
Db 137 PGLQGVKGHAGKRGILGDPGHQKPGKGDVGASGEQGIGP 178

Search completed: August 11, 2005, 08:24:58
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: August 11, 2005, 08:19:50 ; Search time 59 Seconds
(without alignments)
1145.669 Million cell updates/sec

Title: US-10-643-836-297

Perfect score: 703

Sequence: 1 MEGGAYGACGAGFDPYTL.....GEPHPAGTCTESTGCGPQ 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	82.1	234	1 SNG1_HUMAN	O43759 homo sapien
2	550	78.2	234	1 SNG1_MOUSE	O55100 mus musculus
3	547	77.8	234	1 SNG1_RAT	O62876 rattus norv
4	500	71.1	231	2 Q8UW67	Q8UW67 xenopus lae
5	362	51.5	229	1 SNG3_MOUSE	Q8R191 mus musculus
6	353	50.2	229	1 SNG3_HUMAN	O43761 homo sapien
7	306	43.5	219	2 Q6DIE7	Q6DIE7 xenopus tro
8	304	43.2	217	2 Q6AZR4	Q6AZR4 xenopus lae
9	296	42.1	224	1 SNG2_HUMAN	O43760 homo sapien
10	289.5	41.2	294	2 Q7QHR6	Q7QHR6 anopheles g
11	287	40.8	145	2 Q96L30	Q96L30 homo sapien
12	286	40.7	241	2 Q9V6U3	Q9V6U3 drosophila
13	282	40.1	234	1 SNG2_RAT	O54980 rattus norv
14	274	39.0	224	1 SNG2_MOUSE	O55101 mus musculus
15	274	39.0	224	2 Q8CZ25	Q8CZ25 mus musculus
16	274	39.0	224	2 Q99K83	Q99K83 mus musculus
17	211	30.0	191	2 Q6S8R7	Q6S8R7 homo sapien
18	190	27.3	237	1 SNG1_CAEEL	O76735 caenorhabdi
19	170	24.2	243	1 SNG4_MOUSE	O76735 mus musculus
20	169	24.0	234	1 SNG4_HUMAN	O95473 homo sapien
21	167.5	23.8	236	2 Q8E8E8	Q8E8E8 xenopus lae
22	85	12.1	626	2 Q9NHW1	Q9NHW1 nephila ina
23	84.5	12.0	235	2 Q6PEJ1	Q6PEJ1 brachydanio
24	82.5	11.7	202	2 Q853G7	Q853G7 mycobacteri
25	82	11.7	462	2 Q3NHW3	Q3NHW3 nephila cla
26	82	11.7	907	2 Q44359	Q44359 nephila cla
27	81.5	11.6	161	2 Q2KDP9	Q2KDP9 rhizobium m
28	80	11.4	468	1 PTMB_BACHD	Q9K678 bacillus ha
29	79.5	11.3	538	2 Q8H4H5	Q8H4H5 oryza sativ
30	78	11.1	392	1 GOST_CHICK	P28337 gallus gall
31	77.5	11.0	650	2 Q6LKE4	Q6LKE4 photobacter

RESULT 1
SNG1_HUMAN STANDARD; PRT; 234 AA.
AC O43759; O43757; O43758; Q96J56; Q9UGZ4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-1.
GN Name=SYNGR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98430994; PubMed=9760194;
RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dumanski J.P.;
RT "Characterization of the human synaptogyrin gene family.";
RL Hum. Genet. 103:131-141(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Colley V.B., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J.J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spraggon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams H., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Asakawa K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

ALIGNMENTS

32	76	10.8	251	2	Q7ZNV8	Q7ZNV8 xenopus lae
33	76	10.8	288	2	Q6ZM74	Q6ZM74 brachydanio
34	76	10.8	439	2	Q731J4	Q731J4 bacillus ce
35	76	10.8	519	2	Q7NFW8	Q7NFW8 gloeobacter
36	75.5	10.7	232	2	Q6TLG1	Q6TLG1 brachydanio
37	75.5	10.7	348	1	Y479_MYCTU	P64699 mycobacteri
38	75.5	10.7	348	1	Y489_MYCBO	P64700 mycobacteri
39	75.5	10.7	460	2	Q6P2P0	Q6P2P0 homo sapien
40	75.5	10.7	530	1	MATP_HUMAN	Q9UNX9 homo sapien
41	75	10.7	249	2	Q946I4	Q946I4 oryza sativ
42	75	10.7	249	2	Q7G6Z4	Q7G6Z4 oryza sativ
43	75	10.7	439	2	Q635H8	Q635H8 bacillus ce
44	75	10.7	439	2	Q818Y3	Q818Y3 bacillus ce
45	75	10.7	439	2	Q81MC4	Q81MC4 bacillus th
46	75	10.7	439	2	Q6HE62	Q6HE62 bacillus th
47	75	10.7	667	2	Q8VUH1	Q8VUH1 streptococc
48	75	10.7	760	2	Q6BLQ5	Q6BLQ5 debaryomyce
49	74.5	10.6	533	2	Q73FF3	Q73FF3 bacillus ce
50	74.5	10.6	533	2	Q81VY5	Q81VY5 bacillus an

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latrelle P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Serousi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilaahun Y., Wright H.;
RA "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1B).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickens M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1A;
CC IsoId=O43759-1; Sequence=Displayed;
CC Name=1B;
CC IsoId=O43759-2; Sequence=VSP_006332;
CC Name=1C;
CC IsoId=O43759-3; Sequence=VSP_006331, VSP_006332;
CC -!- SIMILARITY: Belongs to the synaptogyrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; AJ002305; CAA05322.1; -;
CC EMBL; AJ002304; CAA05321.1; -;
CC EMBL; AJ002303; CAA05320.1; -;
CC EMBL; AL022326; CAA18451.1; -;
CC EMBL; AL022326; CAA18451.1; -;
CC EMBL; AL022326; CAA18451.1; -;
CC EMBL; BC000731; AAH00731.1; -;
CC Genew; HGNC:11498; SYNGRI.
CC H-InvDB; HIX0016490; -;
CC MIM; 603925; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC InterPro; IPR008253; Marvel.

DR Pfam; PF01284; MARVEL; 1.
KW Alternative splicing; Synapse; Transmembrane.
FT TRANSMEM 24 44 Potential.
FT TRANSMEM 72 92 Potential.
FT TRANSMEM 104 124 Potential.
FT TRANSMEM 149 169 Potential.
FT VARSPLIC 1 33 MEGGAGAGKAGGAFDPYTLVRQPHILRVSW -> MLTL
FT EFGILEPDPSPSWTQSRWSRSPGCE (in
FT isoform 1C).
FT /FTId=VSP_006331.
FT AQAVALFQRYQIGADSAFSDYNDPQSDSMPYAPYVEP
FT NTGPDAGMGTYQQPANTFTPEQGYOQGY -> SLTAA
FT LAVRRFKDLSFOEYSTLFPASAQ (in isoform 1B
FT and isoform 1C).
FT /FTId=VSP_006332.
FT Missing (in Ref. 2).
FT CONFLICT 203 203
SQ SEQUENCE 234 AA; 25570 MW; 8B015CBEBD461E12 CRC64;
Query Match 82.1%; Score 577; DB 1; Length 234;
Best Local Similarity 99.1%; Pred. No. 1.7e-46;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEGGAGAGKAGGAFDPYTLVRQPHILRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60
Db |||||
1 MEGGAGAGKAGGAFDPYTLVRQPHILRVSWLFSIVVFGSIVNKGYNLSASEGEQFCI 60
QY 61 YNRNPACSYGVAVGLAFLTCLLYLALDVYFPQISSVKORKKAVLSDIGVS 112
Db |||||
61 YNRNPACSYGVAVGLAFLTCLLYLALDVYFPQISSVKORKKAVLSDIGVS 112
RESULT 2
SNGI_MOUSE
ID SNGI_MOUSE STANDARD; PRT; 234 AA.
AC 055100; Q9DCB0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-1.
GN Name=Syngrl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORM 1B).
RX MEDLINE=98430994; PubMed=9760194;
RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
RA Collins J.B., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dumaneki J.P.;
RT "Characterization of the human synaptogyrin gene family.";
RL Hum. Genet. 103:131-141(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaudo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 Nature 420:563-573 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1A;
 CC IsoId=O55100-1; Sequence=Displayed;
 CC Name=1B;
 CC IsoId=O55100-2; Sequence=VSP_006333;
 CC -1- SIMILARITY: Belongs to the synaptogyrin family.

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 EMBL; AJ002306; CAA05323.1; -
 EMBL; AK002972; BAB22487.1; -
 EMBL; AK010442; BAB26943.1; -
 MGD; MGI:1328323; Syngri1.
 InterPro; IPR008253; Marvel.
 Pfam; PF01284; MARVEL; 1.
 Alternative splicing; Synapse; Transmembrane.
 TRANSMEM 24 44 Potential.
 TRANSMEM 72 92 Potential.
 TRANSMEM 104 124 Potential.
 TRANSMEM 149 169 Potential.
 VARSPLIC 162 234
 AGQAVLAFORQIGADSLFSDYMDPSQSSMPYAPYVPEP
 SAGSDPAGMGTVQHPANAFDAEPQYQSOGY -> SLTAA
 LAVRRFKELTFQSEYNTLFPASAPQ (in isoform 1B).
 /FTID=VSP_006333.
 SQ SEQUENCE 234 AA; 25653 MW; 09566021DF3B809A CRC64;
 Query Match 78.2%; Score 550; DB 1; Length 234;
 Best Local Similarity 93.8%; Pred. No. 6.1e-44;
 Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLIRVVVSWLFSIVVFGSIVNEGILNSASEGEQFCI 60
 Db 1 MEGGAYGAGKAGGAGDPYTLVRQPHITLIRVVVSWLFSIVVFGSIVNEGILNPPEEEFCCI 60
 QY 61 YNRPNACSYGAVGVLAFLTCLLYLALDVFYFPOISSVKORKKAVLSDIGVS 112
 Db 61 YNRPNACSYGTVGVLAFLTCLLYLALDVFYFPOISSVKORKKAVLSDIGVS 112
 RESULT 3
 SNG1 RAT
 ID SNG1 RAT STANDARD; PRT; 234 AA.
 AC Q62876;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Synaptogyrin-1 (p29).
 GN Name=Syngri1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI TaxID=10116;

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QY 1 MEGGAYGAGKAGGAFDPYTLVROPHTLRVSWLFSIVVFGSIVNEGYNSASEGEQFCI 60
DB 1 MEGGAYGAGKAGGAFDPQFIQPHILRMVSWFSIVVFGIINEGYNSTEEEHCI 60
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDIGVS 112
DB 61 FNRNPACSYGVTVGVLAFLTCLLYLALDVYFPQISSVKDRKKTVIDIAVS 112

RESULT 5
SNG3 MOUSE
ID SNG3 MOUSE STANDARD; PRT; 229 AA.
AC Q8R191; Q9VWG8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Synaptogyrin-3.
GN Name=Syngr3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315823; PubMed=10383386; DOI=10.1074/jbc.274.27.18893;
RA Sugita S., Janz R., Suedhof T.C.;
RT "Synaptogyrins regulate Ca2+-dependent exocytosis in PC12 cells.";
RL J. Biol. Chem. 274:18893-18901(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima I., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to the synaptogyrin family.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF117207; AAD28556.1; -
CC EMBL; AK048753; BAC33444.1; -
CC EMBL; AK081164; BAC38151.1; -
CC EMBL; AK082167; BAC38430.1; -
CC EMBL; BC025022; AAB25022.1; -
CC MGD; MGI:1341881; Syngr3.
CC DR InterPro; IPR008253; Marvel.
CC DR Pfam; PF01284; MARVEL; 1.
CC KW Transmembrane
CC FT TRANSMEM 30 50 Potential.
CC FT TRANSMEM 70 90 Potential.
CC FT TRANSMEM 105 125 Potential.
CC FT TRANSMEM 148 168 Potential.
CC FT CONFLICT 171 171 F -> L (in Ref. 1).
CC SQ SEQUENCE 229 AA; 24561 MW; E04C00555B8A3C08 CRC64;
Query Match 51.5%; Score 362; DB 1; Length 229;
Best Local Similarity 59.3%; Pred. No. 3.7e-26;
Matches 67; Conservative 20; Mismatches 26; Indels 0; Gaps 0;
QY 1 MEGGAYGAGKAGGAFDPYTLVROPHTLRVSWLFSIVVFGSIVNEGYNSASEGEQFCI 60
DB 1 MEGAGFGAGRAGAFDPVSRPOTLLRVVSWFSIAVFGPIVNEGYNSGGPELRVCV 60
QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDIGVS 113
DB 61 FNRNPACSYGVTVGVLAFLTCLLYLALDVYFPQISSVKDRRRAVLLDLGFSS 113

RESULT 6
SNG3 HUMAN
ID SNG3 HUMAN STANDARD; PRT; 229 AA.
AC Q43761;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-3.
GN Name=SYNGR3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98430994; PubMed=9760194;
RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
RA Collins J.B., Dunham I., Blennow E., Roe B.A., Piehl F.,
RA Dumanski J.P.;
RT "Characterization of the human synaptogyrin gene family.";
RL Hum. Genet. 103:131-141(1998).
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[2]
RN REVISIONS.
RP Kedra D.,
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: Expressed in brain and placenta.
CC -|- SIMILARITY: Belongs to the synaptogyrin family.
CC
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CC
CC
CC EMBL; AJ002309; CAA05326.2; -.
CC EMBL; BC014087; AAH14087.1; -.
CC GenBank; U00000.1; SYNGR3.
CC H-InvDB; HIX0012708; -.
CC MIM; 603927; -.
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC InterPro; IPR008253; Marvel.
CC Pfam; PF01284; MARVEL; 1.
CC Transmembrane.
CC TRANSMEM 30 50 Potential.
CC TRANSMEM 70 90 Potential.
CC TRANSMEM 105 125 Potential.
CC TRANSMEM 148 168 Potential.
CC SEQUENCE 229 AA; 24555 MW; 0755812EDD4AD4C5 CRC64;
Query Match 50.2%; Score 353; DB 1; Length 229;
Best Local Similarity 58.4%; Pred. No. 2.6e-25;
Matches 66; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
Qy 1 MEGAGYAGKAGGAFDPVTLVRQPHHTLRVSVWLFSLVFGSIIVNEGVLNSASGEQFCI 60
Db 1 MEGASFGAGRGAALDPVSVFARRQTLRLVASWFSIAVFGPIVNEGIVNTDGPRLCV 60
Qy 61 YNRNPNACSYGVAAGVLAFLTCLLYLALDVYFPQISSVKDKKAVLSDIGVSG 113
Db 61 FNGNAGACRFVGLGFLGFLAFLLDVRFQISSVRDRRAVLLDLGFSG 113
RESULT 7
Q6DIE7 PRELIMINARY; PRT; 219 AA.
AC Q6DIE7
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Syngn2-prov protein.
GN Name=syngn2-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1] _
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075595; AAH75595.1; -.
DR GO; GO:0016020; C: membrane; IEA.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
DR SEQUENCE 219 AA; 24372 MW; 93C4618D9CEFA542 CRC64;
Query Match 43.5%; Score 306; DB 2; Length 219;
Best Local Similarity 49.1%; Pred. No. 7e-21;
Matches 55; Conservative 25; Mismatches 32; Indels 0; Gaps 0;
Qy 1 MEGGAYGAGKAGGAFDPVTLVRQPHHTLRVSVWLFSLVFGSIIVNEGVLNSASGEQFCI 60
Db 1 MEGSAGYAGKAGGAGSFLNFKRPETILRIISCFALIVFACIVSDGYTNPNESKLTCI 60
Qy 61 YNRNPNACSYGVAAGVLAFLTCLLYLALDVYFPQISSVKDKKAVLSDIGVS 112
Db 61 FKNKNDACHYGVGIGFLAFLACILFLFLDLYLTLSNANYRKIVLADLGFS 112
RESULT 8
Q6AZR4 PRELIMINARY; PRT; 217 AA.
AC Q6AZR4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Syngn2-prov protein.
GN Name=syngn2-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.


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SQ SEQUENCE 224 AA; 24810 MW; EC92C95CE9E5BD41 CRC64;
Query Match 42.1%; Score 296; DB 1; Length 224;
Best Local Similarity 48.6%; Pred. No. 6.4e-20;
Matches 53; Conservative 19; Mismatches 37; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSWLFSIVVFGSIVNEGYNLSASEGEQFCI 60
DB 1 MESGAYGAKAGSGDFLRFLTPQVQVARVCLVFLVIFVFCYIGEGYSNAHESKQMYCV 60

QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQISSVKDRKAVLSDI 109
DB 61 FNRNEDACRYGSAIGVLAFLAGAFLLVVDAYFPQISNATDRKYLVIQDL 109

RESULT 10
ID Q7QHR6 PRELIMINARY; PRT; 294 AA.
AC Q7QHR6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP7107 (Fragment)
GN Name=agCG48315; ORFNames=ENSANGG00000015977;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anophelinae.
OX NCBI_TaxID=180454;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008816; EAA05258.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; MARVEL.
DR Pfam; PF01284; MARVEL; 1.
FT NON TER 1
SQ SEQUENCE 294 AA; 33098 MW; 4671F09266A3C730 CRC64;

Query Match 41.2%; Score 289.5; DB 2; Length 294;
Best Local Similarity 42.9%; Pred. No. 3.4e-19;
Matches 60; Conservative 21; Mismatches 28; Indels 31; Gaps 2;

QY 3 GGAYGAGKAGGAFDPYTLVRQPHITLRVSW- 33
DB 21 GGAYGAGKAGGAFDPYTLVRQPHITLRVSW- 80

QY 34 -LFSIVVFGSIVNEGYNLSASEGEQFCIYNRNPNACSYGVAVGVLAFLTCLLYLALDVYF 92
DB 81 PLFAIIIVFGCISSEGMREAN-GKEYCIIIRDGNACNAYGVIGVIAFLAAMGFIAEYLF 139

QY 93 PQISSVKDRKAVLSDIGVS 112
DB 140 EQMSSVTRKHVYLDIGFS 159

RESULT 11
ID Q96L30 PRELIMINARY; PRT; 145 AA.
AC Q96L30;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNGR3 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 11
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RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diachenko L., Marudina K., Farmer A.A., Rubin G.M., Hsieh T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 12;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009568; AAH09568.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; MARVEL.
DR Pfam; PF01284; MARVEL; 1.
SQ SEQUENCE 145 AA; 15164 MW; A23BE7A9BC953CA3 CRC64;

Query Match 40.8%; Score 287; DB 2; Length 145;
Best Local Similarity 56.4%; Pred. No. 3e-19;
Matches 53; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGGAFDPYTLVRQPHITLRVSWLFSIVVFGSIVNEGYNLSASEGEQFCI 60
DB 1 MEGAGGAGGAGGAALDPVSPAREPQTLRLVASVFSIAVFGPIVNEGYNVNTDSGPRLCV 60

QY 61 YNRNPNACSYGVAVGVLAFLTCLLYLALDVYFPQ 94
DB 61 FNGNAGACRFGVALGLGAFACAAFLLLDVRFOQ 94

RESULT 12
ID Q9V6U3 PRELIMINARY; PRT; 241 AA.
AC Q9V6U3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 23-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG10808-PA (RH60941p).
GN Name=synaptotagmin; ORFNames=CG10808;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M.B., Cawley S., Dahlike C., Davenport L.B., Davies P.,
de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslø C., Gabriëlian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodagett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003817; AAF58329.1; -;
DR EMBL; AY071753; AAL49375.1; -;
DR FlyBase; FBgn003876; synaptogyrin.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
SQ SEQUENCE 241 AA; 26610 MW; CFCBAID44450E86A CRC64;

Query Match 40.7%; Score 286; DB 2; Length 241;
Best Local Similarity 47.3%; Pred. No. 6e-19;
Matches 52; Conservative 24; Mismatches 32; Indels 2; Gaps 1;

QY 3 CGAYGAGKAGGAFDPTLVROPHHTLVVSWLFSIVVFGSIVNGLNSASGEQFCIYN 62
DB 13 GGAYGGKAGGAFDPTLVROPHHTLVVSWLFSIVVFGSIVNGLNSASGEQFCIYN 70
QY 63 RNPNCACSYGAVGVGLAFLTLCLLYLALDVVFPQISSVKDKRKKAVLSDIGVS 112
DB 71 GPGMACKGNMVGTVGFLASMGFGGELFERMSSVSKSKRYVMADMGS 120

RESULT 13
SNG2 RAT
ID SNG2 RAT STANDARD; PRT; 234 AA.
AC O54980;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-2 (Cellugyrin).
GN Name-Syng2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112834; PubMed=9446595; DOI=10.1074/jbc.273.5.2851;
RA Janz R., Suedhof T.C.;
RT "Cellugyrin, a novel ubiquitous form of synaptogyrin that is
phosphorylated by pp60(c-src).";
RL J. Biol. Chem. 273:2851-2857(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Ubiquitous, low expression in brain.
CC -!- PTM: Tyrosine phosphorylated by Src.
CC -!- SIMILARITY: Belongs to the synaptogyrin family.
CC
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CC
DR EMBL; AF039085; AAB96666.1; -;
DR RGD; 621334; Syng2.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KW Phosphorylation; Transmembrane.
FT TRANSMEM 40 60 Potential.
FT TRANSMEM 83 103 Potential.
FT TRANSMEM 115 135 Potential.
FT TRANSMEM 157 177 Potential.
SQ SEQUENCE 234 AA; 25709 MW; 68168A78CCF5B8C CRC64;

Query Match 40.1%; Score 282; DB 1; Length 234;
 Best Local Similarity 47.7%; Pred. No. 1.4e-18;
 Matches 52; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGADPDYTLVQPHITLIRVSWLFSIVVFGSIVNEGYNLSASEGEQFCI 60
 DB 11 MEGGAYGAANAGGSFDRIRYSQPVVTRLVSWLALIVFCIFGEGYINLHSSDQLHCV 70

QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVFPQISSVKDRKKAVLSDI 109
 DB 71 FNRNEDACRYGSAIGVLAFLASAFFLVDAFFSQISNATDRKYLVIIGDL 119

RESULT 14
 SNG2_MOUSE STANDARD; PRT; 224 AA.

AC O55101;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Synaptogyrin-2 (Cellugyrin).
 GN Name-Syng2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98430994; PubMed=9760194;
 RA Kedra D., Pan H.-Q., Seroussi E., Fransson I., Guilbaud C.,
 RA Collins J.E., Dunham I., Blennow E., Roe B.A., Piehl F.,
 RA Dumanski J.P.,
 RA "Characterization of the human synaptogyrin gene family.";
 RL Hum. Genet. 103:131-141(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98430994; PubMed=9760194;
 RA Sun M.Y., Reay P.A.;
 RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RL -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the synaptogyrin family.

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DR EMBL; AJ002307; CAA05324.1; -;
 DR EMBL; AF151985; AAD38046.1; -;
 DR MGD; MGI:1328324; Syng2.
 DR InterPro; IPR008253; Marvel.
 DR Pfam; PF01284; MARVEL; 1.
 KW Transmembrane.
 FT TRANSMEM 31 51 Potential.
 FT TRANSMEM 72 92 Potential.
 FT TRANSMEM 105 125 Potential.
 FT TRANSMEM 147 167 Potential.
 SQ SEQUENCE 224 AA; 24778 MW; 951FE014C9C3EEB6 CRC64;

Query Match 39.08; Score 274; DB 1; Length 224;
 Best Local Similarity 45.0%; Pred. No. 7.7e-18;
 Matches 49; Conservative 22; Mismatches 38; Indels 0; Gaps 0;

QY 1 MEGGAYGAGKAGADPDYTLVQPHITLIRVSWLFSIVVFGSIVNEGYNLSASEGEQFCI 60
 DB 1 MEGGAYGAANAGGSFDRIRYSQPVVTRLVSWLALIVFCIFGEGYINLHSSDQLHCV 60

QY 61 YNRNPACSYGVAVGVLAFLTCLLYLALDVFPQISSVKDRKKAVLSDI 109
 DB 61 FNRNEDACRYGSAIGVLAFLASAFFLVDAFFSQISNATDRKYLVIIGDL 109

RESULT 15
 O8C225 PRELIMINARY; PRT; 224 AA.

ID O8C225;
 AC O8C225; (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 25, Last annotation update)
 DE Mus musculus B6-Derived CD11 +ve dendritic cells cDNA, RIKEN full-
 DE length enriched library, clone:F730026A20 product:synaptogyrin 2, full
 DE insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RA "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RA 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RA "Normalization and subtraction of cap-trapper-selected cDNAs to
 RA prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa E., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RA sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tgami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,


```
QY 21 VRQPHILRWVSLFVIVVSGVIVNGLNSASEGEQFCIYNPNACSVGVAVGLAF 80
Db 19 LRRPKSIRIFGVFSLVIFSSLLTDGYQNRTPSQRLCVLNSHNHMACSFVAGGLFSL 78
QY 81 TCLLYLALDVY 91
Db 79 SCLVFLAIDAY 89

RESULT 20
SNG4_HUMAN STANDARD; PRT; 234 AA.
AC Q95473;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Synaptogyrin-4.
GN Name=SYNGR4;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kedra D., Dumanaki J.P.;
RT "Cloning of a novel member of synaptogyrin gene family.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the synaptogyrin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ011733; CAA09754.1; -.
DR Genew; HGNC:11502; SYNGR4.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
KW Transmembrane.
FT TRANSMEM 25 45 Potential.
FT TRANSMEM 66 86 Potential.
FT TRANSMEM 104 124 Potential.
FT TRANSMEM 145 165 Potential.
SQ SEQUENCE 234 AA; 25786 MW; 801134E4D840288F CRC64;

Query Match 24.0%; Score 169; DB 1; Length 234;
Best Local Similarity 38.6%; Pred. No. 6.9e-08;
Matches 34; Conservative 16; Mismatches 38; Indels 0; Gaps 0;

QY 21 VRQPHILRWVSLFVIVVSGVIVNGLNSASEGEQFCIYNPNACSVGVAVGLAF 80
Db 19 LRRPKTITRFVGVFSLVIFSSLLTDGYQNMESPOLCILNLSNVACSFVAGGLAF 78
QY 81 TCLLYLALDVYFPQISVDRKKAVLSD 108
Db 79 SCLAFVLDTQETRIAGTRKTAFLD 106

RESULT 21
Q68ES8 PRELIMINARY; PRT; 236 AA.
AC Q68ES8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE LOC446291 protein (Fragment).
GN Names=LOC446291;
OS Xenopus laevis (African clawed frog).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altshuler S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RX Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC080122; AAH80122.1; -.
DR InterPro; IPR008253; Marvel.
DR Pfam; PF01284; MARVEL; 1.
FT NON_TER 1
SQ SEQUENCE 236 AA; 25738 MW; C1AE117F82DEAA7C CRC64;

Query Match 23.8%; Score 167.5; DB 2; Length 236;
Best Local Similarity 34.3%; Pred. No. 9.6e-08;
Matches 37; Conservative 20; Mismatches 46; Indels 5; Gaps 1;

QY 6 YGAGKAGGAFDPYTLVRQPHILRWVSLFVIVVSGVIVNGLNSASEGEQFCIYNPNP 65
Db 9 FSAAKSGAPSGLVDFIRRPVILRSSILTSIIIVGAV-----SSGCKTHDVCIFNGS 63
QY 66 NCACSGVAVGLAFITCLLYLALDVYFPQISVDRKKAVLSDIGVSG 113
Db 64 SPCSCLAVATGVFAFLGSVAFVDSYMFNSISNKRMRVVMGDLAFSG 111

RESULT 22
Q9NHW1 PRELIMINARY; PRT; 626 AA.
AC Q9NHW1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Flagelliform silk protein (Fragment).
GN Name=Flag;
OS Nephila inaurata madagascariensis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Tetragnathidae; Nephila.
```


sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPr); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to the sugar (By similarity).

-I- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphate.

-I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-I- SIMILARITY: Contains 1 PTS EIIIC domain.

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EMBL: AP001520; BAB07573.1; -
PIR: F84131; F84131.
InterPro: IPR003352; Ptrans_EIIC.
InterPro: IPR003501; Ptrans_IIB.
InterPro: IPR004718; PTSIIC_mtlA.
Pfam: PF023378; PTS_EIIC; 1.
Pfam: PF02302; PTS_IIB; 1.
TIGRFAMs: TIGR00851; mtlA; 1.
KW Complete proteome; Phosphorylation; Phosphotransferase system;
KW Sugar transport; Transferase; Transmembrane.
FT DOMAIN 1 335 EIIB.
FT TRANSMEM 336 468 Potential.
FT TRANSMEM 20 40 Potential.
FT TRANSMEM 50 70 Potential.
FT TRANSMEM 93 113 Potential.
FT TRANSMEM 137 157 Potential.
FT TRANSMEM 163 183 Potential.
FT TRANSMEM 215 235 Potential.
FT TRANSMEM 269 289 Potential.
FT TRANSMEM 290 310 Potential.
FT TRANSMEM 316 336 Potential.
FT MOD RES 258 258 Phosphohistidine (By similarity).
FT MOD RES 386 386 Phosphocysteine (By similarity).
SQ SEQUENCE 468 AA; 49037 MW; 7B0FDA747E75DEB8 CRC64;

Query Match 11.4%; Score 80; DB 1; Length 468;
Best Local Similarity 28.1%; Pred. No. 36;
Matches 36; Conservative 13; Mismatches 49; Indels 30; Gaps 6;

QY 11 AGGAFD---PYTLVQPHITLTVV---SMLFSIVVFGSIVNEGYLNSASEGQFCIYNR 63
Db 254 AGGIHEIYFPYLMK-PTLILAVTAGMSGVFTPLV---NAGLVAVPFGSIFALLAM 308

QY 64 NPACSYGVAVGVLAFLTCLLYLALDYVFPQISSVKDKKAVLSIDIGVSGEPHPAGPCT 123
Db 309 TPREGYAGVLAVI-----IATVSFVIASIIKTSKATBDL-----TEAT 350

QY 124 ESTEGCPG 131
Db 351 SKMEGLKG 358

RESULT 29
Q8H4H5
AC Q8H4H5; PRELIMINARY; PRT; 538 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative Nrampl protein (Putative NRAMPL-like protein).
GN Name=QJ1057_E05.110; Synonyms=Nrampl;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 7, BAC clone:OJ1057_E05.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gross J., Stein R.J., Fett-Neto A.G., Fett J.P.;
RT "Iron homeostasis related genes in rice.";
RL Genet. Mol. Biol. 26:477-497(2003).
DR EMBL: AP004176; BAC21413.1; -
DR EMBL: BK000593; DAA01394.1; -
DR Gramene; Q8H4H5; -
DR GO: GO:0016020; C.membrane; IEA.
DR GO: GO:0005215; F.transporter activity; IEA.
DR GO: GO:0006810; P.transport; IEA.
DR InterPro: IPR001046; Nrampl.
DR Pfam: PF01566; Nrampl; 1.
DR PRINTS; PR00447; NATHESASSCMP.
DR PRODOM; PD001861; Nrampl; 1.
DR TIGRFAMs; TIGR01197; nrampl; 1.
SQ SEQUENCE 538 AA; 58497 MW; B07763D611234327 CRC64;

Query Match 11.3%; Score 79.5; DB 2; Length 538;
Best Local Similarity 24.7%; Pred. No. 46;
Matches 37; Conservative 25; Mismatches 47; Indels 41; Gaps 9;

QY 3 GGAYGAGK-----AGGAFD-PYTLV-----RQPH---TILRVVSWLFSIVVFG 41
Db 383 GSGRGAGRLIIITIASMILSPFLPALLKLFSSSKSMGPKNSIYIVFSWFLGLLIIG 442

QY 42 SIVNEGYLNSASEGQFCIYNRNPACSYGVAVGVLAFLTCLLYLALDYV----- 92
Db 443 --INMYFLSTSFVG--WLHNDLPKYAN--VLGAAVFPMLVYIVAVVYLTIRKDSVVT 496

QY 93 ----POISSVKDKKAVLSIDIGV-SGEPHP 117
Db 497 FVADSSLAADVDAEKADAGDLAVDDDEPLP 526

RESULT 30
GCST_CHICK
ID GCST_CHICK STANDARD; PRT; 392 AA.
AC P28337;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine cleavage system T protein) (GCVT).
DE Name=AMT;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoeauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92406724; PubMed=1526969;
RA Okamura-Ikeda K., Fujiwara K., Motokawa Y.;
RT "Molecular cloning of a cDNA encoding chicken T-protein of the glycine cleavage system and expression of the functional protein in Escherichia coli. Effect of mRNA secondary structure in the translational initiation region on expression.";
RL J. Biol. Chem. 267:18284-18290(1992).
RN [2]
RP SEQUENCE OF 179-392 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91161577; PubMed=2002038;
RA Okamura-Ikeda K., Fujiwara K., Yamamoto M., Hiraga K., Motokawa Y.;

SEQUENCE FROM N.A.
RC Tissue=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046866; AAH4686.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
SQ SEQUENCE 251 AA; 28297 MW; 436354C6D8330E21 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 251;
Best Local Similarity 23.5%; Pred. No. 47;
Matches 36; Conservative 23; Mismatches 46; Indels 48; Gaps 7;

QY 3 GGAYGAGKAGGADPVTLR-----OPHTILRVVWLFISIVVFGSIVN-----45
DB 5 GGLAGLGKK-----NPPAGLRWRLEPLGFKLLEWLFAPFGSCGSGSETAATVMCK 60

QY 46 -----ECYLSASEGQFCYNNRNPN--AC-----SYGVAVGVLAFL 80
DB 61 SEADTEIKLISVFPFGFYRLRYORYEMPACDDMERRILHLTGDFSAFAPFFVTMGVFAFL 120

QY 81 TCLLYLALDVYFPQISSVKDKKAVLSLDIGVSG 113
DB 121 YAMFALVILVLRPHE-EYTKIRLPIV-DLCVTG 151

RESULT 33
Q6ZM74 PRELIMINARY; PRT; 288 AA.
AC Q6ZM74;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE SI:zk70P6.6 (Novel protein similar to vertebrate synaptophysin (SYP))
DE (Fragment).
GN Names=syp; Synonyms=SI:zk70P6.6;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Beasley H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL831748; CAB50427.1; -
DR ZFIN; ZDB-GENE-031104-2; syp.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 288 AA; 32151 MW; 186010E91045FE20 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 288;
Best Local Similarity 17.6%; Pred. No. 53;
Matches 23; Conservative 28; Mismatches 42; Indels 38; Gaps 4;

QY 18 YTLVRQHTILRVVWLFISIVVF-----GSI-----VN 45
DB 7 FRLVKVPLGFKILEWFAIFAFATCGSYSGSFRMSVECKNRSDNLKIDVDPEYFPLRH 66

SEQUENCE FROM N.A.
RC Tissue=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046866; AAH4686.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
SQ SEQUENCE 251 AA; 28297 MW; 436354C6D8330E21 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 251;
Best Local Similarity 23.5%; Pred. No. 47;
Matches 36; Conservative 23; Mismatches 46; Indels 48; Gaps 7;

QY 3 GGAYGAGKAGGADPVTLR-----OPHTILRVVWLFISIVVFGSIVN-----45
DB 5 GGLAGLGKK-----NPPAGLRWRLEPLGFKLLEWLFAPFGSCGSGSETAATVMCK 60

QY 46 -----ECYLSASEGQFCYNNRNPN--AC-----SYGVAVGVLAFL 80
DB 61 SEADTEIKLISVFPFGFYRLRYORYEMPACDDMERRILHLTGDFSAFAPFFVTMGVFAFL 120

QY 81 TCLLYLALDVYFPQISSVKDKKAVLSLDIGVSG 113
DB 121 YAMFALVILVLRPHE-EYTKIRLPIV-DLCVTG 151

RESULT 33
Q6ZM74 PRELIMINARY; PRT; 288 AA.
AC Q6ZM74;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE SI:zk70P6.6 (Novel protein similar to vertebrate synaptophysin (SYP))
DE (Fragment).
GN Names=syp; Synonyms=SI:zk70P6.6;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Beasley H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL831748; CAB50427.1; -
DR ZFIN; ZDB-GENE-031104-2; syp.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 288 AA; 32151 MW; 186010E91045FE20 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 288;
Best Local Similarity 17.6%; Pred. No. 53;
Matches 23; Conservative 28; Mismatches 42; Indels 38; Gaps 4;

QY 18 YTLVRQHTILRVVWLFISIVVF-----GSI-----VN 45
DB 7 FRLVKVPLGFKILEWFAIFAFATCGSYSGSFRMSVECKNRSDNLKIDVDPEYFPLRH 66

SEQUENCE FROM N.A.
RC Tissue=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046866; AAH4686.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
SQ SEQUENCE 251 AA; 28297 MW; 436354C6D8330E21 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 251;
Best Local Similarity 23.5%; Pred. No. 47;
Matches 36; Conservative 23; Mismatches 46; Indels 48; Gaps 7;

QY 3 GGAYGAGKAGGADPVTLR-----OPHTILRVVWLFISIVVFGSIVN-----45
DB 5 GGLAGLGKK-----NPPAGLRWRLEPLGFKLLEWLFAPFGSCGSGSETAATVMCK 60

QY 46 -----ECYLSASEGQFCYNNRNPN--AC-----SYGVAVGVLAFL 80
DB 61 SEADTEIKLISVFPFGFYRLRYORYEMPACDDMERRILHLTGDFSAFAPFFVTMGVFAFL 120

QY 81 TCLLYLALDVYFPQISSVKDKKAVLSLDIGVSG 113
DB 121 YAMFALVILVLRPHE-EYTKIRLPIV-DLCVTG 151

RESULT 33
Q6ZM74 PRELIMINARY; PRT; 288 AA.
AC Q6ZM74;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE SI:zk70P6.6 (Novel protein similar to vertebrate synaptophysin (SYP))
DE (Fragment).
GN Names=syp; Synonyms=SI:zk70P6.6;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Beasley H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL831748; CAB50427.1; -
DR ZFIN; ZDB-GENE-031104-2; syp.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008021; C:synaptic vesicle; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR008253; Marvel.
DR InterPro; IPR001285; Synaptophysin.
DR Pfam; PF01284; MARVEL; 1.
DR PRINTS; PR00220; SYNAPTOPHYSN.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 288 AA; 32151 MW; 186010E91045FE20 CRC64;

Query Match 10.8%; Score 76; DB 2; Length 288;
Best Local Similarity 17.6%; Pred. No. 53;
Matches 23; Conservative 28; Mismatches 42; Indels 38; Gaps 4;

QY 18 YTLVRQHTILRVVWLFISIVVF-----GSI-----VN 45
DB 7 FRLVKVPLGFKILEWFAIFAFATCGSYSGSFRMSVECKNRSDNLKIDVDPEYFPLRH 66

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RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=146211292;
RA Nakamura Y., Kaneko T., Sato S., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RL cyanoacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
DR EMBL: AF006580; BAC91347.1; -.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0008565; F:protein transporter activity; IEA.
DR GO: GO:0015031; P:protein transport; IEA.
DR InterPro: IPR010432; RDD.
DR InterPro: IPR006260; TonB_C.
DR Pfam: PF06271; RDD; 1.
DR TIGRFAMs: TIGR01352; tonB_Cterm; 1.
KW Complete proteome.
SQ
SEQUENCE 519 AA; 54789 MW; 1756602E3PD37A8D CRC64;

Query Match 10.8%; Score 76; DB 2; Length 519;
Best Local Similarity 19.6%; Pred. No. 95;
Matches 30; Conservative 24; Mismatches 37; Indels 62; Gaps 4;

QY 31 VSWLFSIVVFGSIIVNE-----GYLNSASGEQFCIYNR-----NPNACS----- 69
DB 132 VGVFDSVLFGLLASGFLVLAFIFASLDGKGLDPKFNTRMTIADPRRTSANLYPAIV 191
QY 70 -----YGVAVGVLAFLTCLLYLALDVVFPQI----- 95
DB 192 SSILFILLVAAVLAIIPLFLFALNIKFELTPEPPAPSMWFTLTDPTDKVKPPEN 251
QY 96 -----SSVDRKKAVLSIDIGVSGHPAGTP 121
DB 252 APKSNANSVAKNRQLPTDAGVKGAQPARPTP 284

RESULT 36
Q6TLGI PRELIMINARY; PRT; 232 AA.
ID Q6TLGI
AC Q6TLGI
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Synaptophysin-like protein.
GN ORFNames=wu:fc22a07;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney marrow;
RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY394944; AAC94571.1; -.
DR ZFIN: ZDB-GENE-030131-2940; wu:fc22a07.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008021; C:synaptic vesicle; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR008253; Marvel.
DR InterPro: IPR001285; Synaptophysin.
DR Pfam: PF01284; MARVEL; 1.
DR PRINTS: PR00220; SYNAPTOPHYSIN.
SQ SEQUENCE 232 AA; 25806 MW; 1D55129BEEA9B9CA CRC64;

Query Match 10.7%; Score 75.5; DB 2; Length 232;
Best Local Similarity 25.2%; Pred. No. 48;

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Matches 29; Conservative 16; Mismatches 29; Indels 41; Gaps 4;
QY 21 VRQPHITLRVSVWLFISIVVFG-----SIVNEG-----YLNSSASE 54
DB 11 LKEPLGPIRVLEWIFAFATTTGGYSTGFNVICKSSVTOEINASFSPFRLLTQSY 70
QY 55 GEQFCIYNR-----NPNACSYGAVGVLAFL-----TCLLYLALDVVFPQ 94
DB 71 KVPTCEANSTTFRTRQLTGDHSSAAEFFVAVGVLAFLYSTATLVLYGVQHLRYQ 125

RESULT 37
Y479 MYCTU STANDARD; PRT; 348 AA.
ID Y479 MYCTU
AC P64659; Q11145;
DT 01-OCT-1996 (Rel. 34, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Hypothetical protein Rv0479c/MT0497.
GN OrderedLocusNames=Rv0479c, MT0497; ORFNames=MTCV20G9.05c;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA Teika F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., R.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RT Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL: EX842573; CAB00940.1; -.
DR EMBL: AE000516; AAK44720.1; -.
DR FIC: B70743; B70743.
DR TIGR: MT0497; -.
DR TubercuList: Rv0479c; -.
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 111 131 Potential.
FT TRANSMEM 235 255 Potential.
SQ SEQUENCE 348 AA; 37048 MW; 9EBB7A8CF9E176C1 CRC64;

Query Match 10.7%; Score 75.5; DB 1; Length 348;

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Best Local Similarity 25.2%; Pred. No. 72;
Matches 40; Conservative 19; Mismatches 55; Indels 45; Gaps 7;

QY 7 GAGKAGGADPYTLV-----RQPHILRVVSWLFSIVVFGSIVNVEGY- 48
DB 76 GRQAHAQWDPDTGLLAAQEEBPAAVKTRARRDPLTVFLVLIIVFSLVLAGLIGGELYA 135
QY 49 ---LNSASEGEQFCIYNRPNACSIVGAVGVLAFLTCLLYLALDVVFPQIS-----SVK 99
DB 136 RHVANSKVAQAVCVVKDQATA-SFGVA-----PLLLWQVATRHFTNISVETAGNQIR 187
QY 100 DRK----KAVLSDIGVSGEHPAGT-----PCTESTEG 128
DB 188 DAKGMQIKLTIONVRLKNTPNRGTIGALDATTISSEG 226

RESULT 38
Y489_MYCBO STANDARD; PRT; 348 AA.
AC P64700; Q11145;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Hypothetical protein Mb0489c.
DE OrderedLocusNames=Mb0489c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; BX248335; CAD93352.1; --
KW Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 111 131 Potential.
FT TRANSMEM 235 255 Potential.
SQ SEQUENCE 348 AA; 37048 MW; 9EBB7A8CF9E176C1 CRC64;

Query Match 10.7%; Score 75.5; DB 1; Length 348;
Best Local Similarity 25.2%; Pred. No. 72;
Matches 40; Conservative 19; Mismatches 55; Indels 45; Gaps 7;

QY 7 GAGKAGGADPYTLV-----RQPHILRVVSWLFSIVVFGSIVNVEGY- 48
DB 76 GRQAHAQWDPDTGLLAAQEEBPAAVKTRARRDPLTVFLVLIIVFSLVLAGLIGGELYA 135
QY 49 ---LNSASEGEQFCIYNRPNACSIVGAVGVLAFLTCLLYLALDVVFPQIS-----SVK 99
DB 136 RHVANSKVAQAVCVVKDQATA-SFGVA-----PLLLWQVATRHFTNISVETAGNQIR 187
QY 100 DRK----KAVLSDIGVSGEHPAGT-----PCTESTEG 128
DB 188 DAKGMQIKLTIONVRLKNTPNRGTIGALDATTISSEG 226

RESULT 39
Q6P2PO
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Q6P2PO PRELIMINARY; PRT; 460 AA.
AC Q6P2PO;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE MATP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusi D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064405; AAH64405.1; --
SQ SEQUENCE 460 AA; 51233 MW; 26901FD0438C14DD CRC64;

Query Match 10.7%; Score 75.5; DB 2; Length 460;
Best Local Similarity 28.7%; Pred. No. 94;
Matches 29; Conservative 10; Mismatches 35; Indels 27; Gaps 4;

QY 24 PH----TILRVVSW-----LPSIVVFGSIVNVEGYLNSASEGEQFCIYNRPNACSIVG 72
DB 315 PHRYLCISHLIGWTAFNLNMLFTDFMGQIVTRGDPYSAHNSTFLIYER-----GV 367
QY 73 AVGVLAFLTCLLYLALDVVFPQISSVKDRKKAIVLSDIGVSG 113
DB 368 EVGCWGFCSNVFSSLYSYF-----QKVLVSYIGLKG 399

RESULT 40
MATP_HUMAN STANDARD; PRT; 530 AA.
AC Q6UMT9; Q9BTM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE MATP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM AIM-1A).
RC TISSUE=Melanoma;
RX MEDLINE=21115844; PubMed=11221837;
```

RA Harada M., Li Y.F., El-Gamil M., Rosenberg S.A., Robbins P.F.;
RT "Use of an in vitro immunoselected tumor line to identify shared
RT melanoma antigens recognized by HLA-A*0201-restricted T cells."; <http://www.isb-sib.ch/announce/>
RL Cancer Res. 61:1089-1094(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM AIM-1B).
RX TISSUE=Skin;
RY MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Abramson R.D., Mullany C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Green E.D., Dickinson M.C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."; [http://www.ncbi.nlm.nih.gov/proc/natl/proc/16903\(2002\).](http://www.ncbi.nlm.nih.gov/proc/natl/proc/16903(2002).)
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP ALTERNATIVE SPLICING.
RX Ferro S.;
RY Unpublished observations (NOV-2001).
RN [4]
RP DISEASE, AND VARIANT LEU-374.
RX MEDLINE=21473748; PubMed=11574907;
RA Newton J.M., Cohen-Barak O., Hagiwara N., Gardner J.M., Davison M.T.,
RA King R.A., Brilant M.H.;
RT "Mutations in the human orthologue of the mouse underwhite gene (uw)
RT underlie a new form of oculocutaneous albinism, OCA4."; [http://www.ncbi.nlm.nih.gov/hum/genet/69:981-988\(2001\).](http://www.ncbi.nlm.nih.gov/hum/genet/69:981-988(2001).)
RL Am. J. Hum. Genet. 69:981-988(2001).
CC -/- FUNCTION: Melanocyte differentiation antigen. May transport
CC substances required for melanin biosynthesis (By similarity).
CC -/- SUBCELLULAR LOCATION: Integral membrane protein; melanosome (By
CC similarity).
CC -/- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=AIM-1a;
CC IsoId=O9UMX9-1; Sequence=Displayed;
CC Name=AIM-1b;
CC IsoId=O9UMX9-2; Sequence=VSP_006297, VSP_006298, VSP_006299;
CC Name=AIM-1c;
CC IsoId=O9UMX9-3; Sequence=VSP_006296;
CC -/- TISSUE SPECIFICITY: Expressed in most melanoma cell lines and
CC melanocytes.
CC -/- DISEASE: Defects in MATP are the cause of oculocutaneous albinism
CC type 4 (OCA4) [MIM:606574]. OCA4 is characterized by
CC hypopigmentation of skin, hair and eyes. It leads to reduced
CC visual acuity.
CC -/- SIMILARITY: Belongs to the glycoside-pentoside-hexuronide (GPH)
CC cation symporter transporter (TC 2.A.2) family.
CC -/- CAUTION: Ref.2 sequence differs from that shown due to a
CC frameshift in position 188.
CC -/- CAUTION: The described alternatively spliced isoforms are inferred
CC using information from ESTs.
CC NOTE=Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/matpmut.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF172849; AAD51812.1; -.
DR EMBL; BC003597; AAO03597.1; ALT_FRAME.
DR GenBank; HGNC:16472; MATP.
DR MIM; 606202; -.
DR MIM; 606574; -.
KW Albinism; Alternative splicing; Antigen; Glycoprotein;
KW Melanin biosynthesis; Polymorphism; Transmembrane; Vision.
FT DOMAIN 1 46 Cytoplasmic (Potential).
FT TRANSMEM 47 67 Extracellular (Potential).
FT DOMAIN 68 68 Extracellular (Potential).
FT TRANSMEM 69 89 Extracellular (Potential).
FT DOMAIN 90 110 Cytoplasmic (Potential).
FT TRANSMEM 111 131 Extracellular (Potential).
FT DOMAIN 132 138 Extracellular (Potential).
FT TRANSMEM 139 159 Extracellular (Potential).
FT DOMAIN 160 184 Cytoplasmic (Potential).
FT TRANSMEM 185 205 Extracellular (Potential).
FT DOMAIN 206 216 Extracellular (Potential).
FT TRANSMEM 217 237 Cytoplasmic (Potential).
FT DOMAIN 238 318 Cytoplasmic (Potential).
FT TRANSMEM 319 339 Extracellular (Potential).
FT DOMAIN 340 367 Extracellular (Potential).
FT TRANSMEM 367 387 Extracellular (Potential).
FT DOMAIN 388 398 Cytoplasmic (Potential).
FT TRANSMEM 399 419 Extracellular (Potential).
FT DOMAIN 420 425 Extracellular (Potential).
FT TRANSMEM 426 446 Cytoplasmic (Potential).
FT DOMAIN 447 477 Extracellular (Potential).
FT TRANSMEM 478 498 Extracellular (Potential).
FT DOMAIN 499 504 Extracellular (Potential).
FT TRANSMEM 505 525 Extracellular (Potential).
FT DOMAIN 526 530 Cytoplasmic (Potential).
FT CARBOHYD 356 356 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 129 187 Missing (in isoform AIM-1c).
FT VARSPLIC 188 295 Missing (in isoform AIM-1b).
FT VARSPLIC 386 406 Missing (in isoform AIM-1b).
FT VARSPLIC 407 530 Missing (in isoform AIM-1b).
FT VARIANT 374 374 F -> L.
FT SEQUENCE 530 AA; 58301 MW; F14A4BACAA8FF31B CRC64;
Query Match 10.7%; Score 75.5; DB 1; Length 530;
Best Local Similarity 28.7%; Pred. No. 1.1e+02;
Matches 29; Conservative 10; Mismatches 35; Indels 27; Gaps 4;
QY 24 PH-----TILRVSVW-----LFSIVVFGSIYVNEGVLNSASGEQFCIYRNPNACSYGV 72
Db 315 PHRYLCISHLIGTAFSLNMLFFDTFMQIVYRGDPYSAHNSTEFLIVER-----GV 367
QY 73 AVGVLAFLCLLYLALDVFYFQISSVKDRKKAVLSDIGVSG 113
Db 368 EVGCGWGCINSVFSSLYSYF-----QKVLVSVIGLKG 399
RESULT 41
ID Q94614 PRELIMINARY; PRT; 249 AA.
AC Q94614; Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Alpha-expansin OSEXP18.
GN Name=EXP18;
OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriophartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21521099; PubMed=11641069; DOI=10.1016/S1369-5266(00)00211-9;
RA Lee Y., Choi D., Kende H.;
RT "Expansins: ever-expanding numbers and functions.";
RL Curr. Opin. Plant Biol. 4:527-532(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22315554; PubMed=12428004; DOI=10.1104/pp.008888;
RA Lee Y., Kende H.;
RT "Expression of alpha-expansin and expansin-like genes in deepwater
RT rice.";
RL Plant Physiol. 130:1396-1405(2002).
CC -!- SIMILARITY: Belongs to the expansin family.
DR EMBL: AF394553; AAL24489.1; -.
DR Gramine; O94614; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
DR InterPro; IPR009009; Barwin_like.
DR InterPro; IPR002963; Expansin.
DR InterPro; IPR007112; Expan endogl.
DR InterPro; IPR007118; Expan Lol PI.
DR InterPro; IPR007117; Expan Lol PI C.
DR InterPro; IPR005132; Lipoprotein_13.
DR Pfam; PF03330; DPBB 1; 1.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01226; EXPANSIN.
DR ProDom; PD002179; Expan Lol PI C; 1.
DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
DR PROSITE; PSS0842; EXPANSIN_EG45; 1.
SQ SEQUENCE 249 AA; 26431 MW; B375CC995F08D6E0 CRC64;

Query Match 10.7%; Score 75; DB 2; Length 249;
Best Local Similarity 24.2%; Pred. No. 57;
Matches 23; Conservative 12; Mismatches 22; Indels 38; Gaps 3;

QY 3 GGAYGAGKAGGAFDPYTLVRQPHILRVSVWLSFVFGSIVNEGY-----LN 50
Db 32 GGADSGTGGAGC-----YGNLYDQGYGINNAALSTPLFNN 68

QY 51 SASGEQF---CIYNNPNACSVGVAVGLAFLTC 82
Db 69 GASGCGCYLIICNDYKAPSGCRMGTAITVTGTNFC 103

RESULT 43
Q635H8 PRELIMINARY; PRT; 439 AA.
AC Q635H8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Probable Na+/H+ antiporter.
GN ORFNames=BTZK3859;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RA "Complete genome sequence of Bacillus cereus ZK";
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CP000001; AAU16409.1; -.
SQ SEQUENCE 439 AA; 46439 MW; CBEB3FA565D24194 CRC64;

Query Match 10.7%; Score 75; DB 2; Length 439;
Best Local Similarity 22.1%; Pred. No. 1e+02;
Matches 25; Conservative 30; Mismatches 44; Indels 14; Gaps 4;

QY 28 LRVSVWLSFIVW---FGSIVNE-GYINSASGEQFCIYNNPNACSVGVAVGL----- 77
Db 289 MRWMSFGVWISAGGAVLRKTHGVLSVQSAHIGNKPLAFLMLVIGLVTMGI 348

QY 78 --AFLTCLLYALDVPFPQISSVKDRKAVLSDIGVSGEPHPAGTCTESTEG 128
Db 349 GSSFST--IPILTIFVPLCQLGFSFPMATIAITAGALGDAGSPASDSTLG 399

RESULT 44
Q818Y3 PRELIMINARY; PRT; 439 AA.
AC Q818Y3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transport protein.
GN OrderedLocusNames=BC4103;

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriophartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21521099; PubMed=11641069; DOI=10.1016/S1369-5266(00)00211-9;
RA Lee Y., Choi D., Kende H.;
RT "Expansins: ever-expanding numbers and functions.";
RL Curr. Opin. Plant Biol. 4:527-532(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22315554; PubMed=12428004; DOI=10.1104/pp.008888;
RA Lee Y., Kende H.;
RT "Expression of alpha-expansin and expansin-like genes in deepwater
RT rice.";
RL Plant Physiol. 130:1396-1405(2002).
CC -!- SIMILARITY: Belongs to the expansin family.
DR EMBL: AF394553; AAL24489.1; -.
DR Gramine; O94614; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.
DR InterPro; IPR009009; Barwin_like.
DR InterPro; IPR002963; Expansin.
DR InterPro; IPR007112; Expan endogl.
DR InterPro; IPR007118; Expan Lol PI.
DR InterPro; IPR007117; Expan Lol PI C.
DR InterPro; IPR005132; Lipoprotein_13.
DR Pfam; PF03330; DPBB 1; 1.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01226; EXPANSIN.
DR ProDom; PD002179; Expan Lol PI C; 1.
DR PROSITE; PSS0843; EXPANSIN_CBD; 1.
DR PROSITE; PSS0842; EXPANSIN_EG45; 1.
SQ SEQUENCE 249 AA; 26431 MW; B375CC995F08D6E0 CRC64;

Query Match 10.7%; Score 75; DB 2; Length 249;
Best Local Similarity 24.2%; Pred. No. 57;
Matches 23; Conservative 12; Mismatches 22; Indels 38; Gaps 3;

QY 3 GGAYGAGKAGGAFDPYTLVRQPHILRVSVWLSFVFGSIVNEGY-----LN 50
Db 32 GGADSGTGGAGC-----YGNLYDQGYGINNAALSTPLFNN 68

QY 51 SASGEQF---CIYNNPNACSVGVAVGLAFLTC 82
Db 69 GASGCGCYLIICNDYKAPSGCRMGTAITVTGTNFC 103

RESULT 42
Q7G6Z4 PRELIMINARY; PRT; 249 AA.
AC Q7G6Z4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative alpha-expansin.
GN Name=OSJNBa001114.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriophartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Sasaki C., Henry D., Oates R., Simons J.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the expansin family.
DR EMBL; AC105730; AAM51841.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009664; P:cell wall organization and biogenesis (sens. . .; IEA.

[illegible]

RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Koisoce A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic
adaptations and a large plasmid related to *Bacillus anthracis* pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017264; AAS38989.1; -;
DR TIGR; BCE0053; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; Polysacc synt.
DR Pfam; PF01943; Polysacc synt.
KW Complete proteome.
SQ SEQUENCE 533 AA; 58652 MW; D652376B752A1019 CRC64;

Query Match 10.6%; Score 74.5; DB 2; Length 533;
Best Local Similarity 20.4%; Pred. No. 1.4e+02;
Matches 22; Conservative 24; Mismatches 33; Indels 29; Gaps 4;

QY 27 ILRVSWLFSIVVFGSIVN---EGVLN-----SASE-----GEQFCI 60
Db 125 LLRVISFSLMPPFLSVARGYQGFNNMPTAVSQVIEQTIRVSIIVFLSLFLIAHEFDL 184

QY 61 YNRNPACSYGVAVGVLAFLTCLLYALD---VYRPQISSVKDRKAV 105
Db 185 YTVGAGMLGSIAGGLIGIIVILYMRHDFRSIFFKSVKRIKGGKKII 232

RESULT 50
Q81VY5 PRELIMINARY; PRT; 533 AA.
AC Q81VY5; Q614Y9; Q8KYN3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Stage V sporulation protein B, putative.
GN OrderedLocusNames=BA0054, BAS0054, GEAA0054;
OS *Bacillus anthracis*.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oekstad O.A., Helgason E., Rillstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (May-2004) to the EMBL/GenBank/DBAJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterner;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBAJ databases.
DR EMBL; AE017024; AAP24109.1; -;
DR EMBL; AE017334; AAT29132.1; -;
DR EMBL; AE017225; AAT52392.1; -;
DR TIGR; BAA0054; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR InterPro; IPR002797; Polysacc synt.
DR Pfam; PF01943; Polysacc synt.
KW Complete proteome.
SQ SEQUENCE 533 AA; 58670 MW; 99FC61P7815F81AE CRC64;

Query Match 10.6%; Score 74.5; DB 2; Length 533;
Best Local Similarity 20.4%; Pred. No. 1.4e+02;
Matches 22; Conservative 24; Mismatches 33; Indels 29; Gaps 4;

QY 27 ILRVSWLFSIVVFGSIVN---EGVLN-----SASE-----GEQFCI 60
Db 125 LLRVISFSLMPPFLSVARGYQGFNNMPTAVSQVIEQTIRVSIIVFLSLFLIAHEFDL 184

QY 61 YNRNPACSYGVAVGVLAFLTCLLYALD---VYRPQISSVKDRKAV 105
Db 185 YTVGAGMLGSIAGGLIGIIVILYMRHDFRSIFFKSVKRIKGGKKII 232

Search completed: August 11, 2005, 08:20:57
Job time : 61 secs